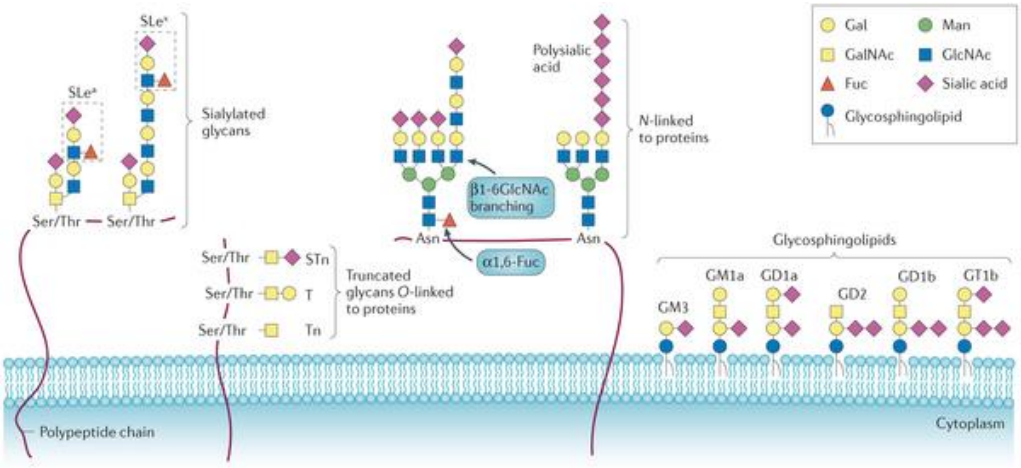


Glycoproteomic Characterization of Bladder Cancer Chemoresistant Cells

Diogo André Teixeira Neves
Mestrado em Bioquímica
Departamento de Química e Bioquímica
2015

Orientador
José Alexandre Ferreira, Professor Doutor, IPO-Porto

Coorientador
André Silva, Doutor, Investigador Auxiliar, Faculdade de Ciências, Universidade do Porto

Todas as correções determinadas pelo júri, e só essas, foram efetuadas.

O Presidente do Júri,

Porto, _____/_____/_____

“Success consists of going from failure to failure without loss of enthusiasm.**”**

Winston Churchill

Dava tudo para te ter aqui, meu querido avô!

1937-2014

Agradecimentos

Foi, sem dúvida, um ano de grande aprendizagem. Não só da aprendizagem do método (sabe sempre a pouco), mas sobretudo da aprendizagem que nos faz crescer enquanto seres íntegros e completos. Um ano que se tornou curto face a tudo aquilo que ainda queria aprender com os melhores.

Ao Professor Doutor José Alexandre Ferreira pela orientação, por toda a disponibilidade e paciência. Muita paciência. Sinto que muitas das vezes o tempo faz com que tenhamos que nos desdobrar em vários campos. No campo possível partilhado por nós, pude perceber que estive perante um grande senhor da Ciência. Fez-me perceber também que o pensamento simples faz mover montanhas e que o complexo não se alcança sem uma boa dose de simplicidade. Vejo-o como um exemplo a seguir, como uma figura de proa no panorama científico. Muito obrigado!

Ao Professor Doutor Luís Lima por toda a ajuda, conhecimento técnico, pela forma didáctica e simples como aborda as situações. Fez-me perceber a simplicidade dos processos, como podemos ser metodológicos e organizados. É fácil trabalhar com pessoas como o Luís! Devo-lhe também um enorme agradecimento!

Ao Doutor André Silva pela co-orientação deste trabalho, pela disponibilidade com que me acolheu e pela interpretação dos espectros de massa.

A todos os meus colegas do Grupo de Patologia e Terapêutica Experimental. Pude aprender um pouco de tudo convosco, pude desfrutar da vossa boa disposição incessante. De todos, não consigo deixar de destacar a Elisabete Fernandes por me ter ao seu cuidado em muitos dos momentos. Obrigada por toda a paciência, consegui aprender muito contigo. Surpreendeste-me muito, vais muito longe!

Ao Professor Doutor Lúcio Lara Santos, coordenador do grupo, por me ter concedido a oportunidade de pertencer ao GPTE e ter lidado com os melhores!

À minha família. Não somos nada sem a nossa família e, felizmente, eu tenho a minha sempre do meu lado independentemente das minhas opções. Queria destacar a minha mãe Glória por ser a minha lutadora e querer sempre o melhor para mim. Obrigado por funcionares como mãe e como pai ao mesmo tempo e por me permitires ser o que sou hoje. Á minha avó Fernanda por estar tão perto de mim, por ser a minha segunda mãe, por estar comigo nos momentos mais importantes da minha vida. Queria destacar também três das mais importantes pessoas da minha vida. Posso nunca ter tido um pai verdadeiramente, mas posso dizer que tive várias figuras que

funcionaram como tal. Ao meu tio Rui por acreditar muito em mim e por estar sempre presente quando preciso. Quando ao longe me vires a tombar, sei que virás a correr segurar-me. Se isto não for dogmático, não acredito em nada. Queria também agradecer ao Vítor, meu padrasto, por ter uma palavra a dizer na minha educação. Também me orgulho muito de te ter presente na minha vida. Finalmente, queria agradecer ao meu avô Álvaro que já partiu. Sei que, do local onde me estás a ver, sorris. Sorris por me veres a cumprir esta etapa. Sorris porque sempre sorriste, mesmo quando não havia razões para sorrir. Nunca te esquecerei, és um exemplo. Quero ser como tu foste!

À minha namorada Cíntia. Quanto te conheço, conheço-me. E quando não me conheço, sei que te conhecendo, reconheço-me. E, o resto, digo-te todos os dias e espero continuar a dizer durante muitos mais.

Uma palavra de apreço à comunidade bioquímica da UP por também ter aprendido e gozado a vida convosco. Em especial, gostaria de destacar o André, a Joana, a Jessica e a Ana. Espero que os nossos caminhos nunca se descruzem!

Por último, a quatro dos melhores do mundo, à minha irmandade. Ao Pedro, ao Rui, ao Fábio e ao Nuno por serem os quatro de sempre, para sempre. A nossa união prevalecerá sempre, nunca se esqueçam disso!

Resumo

O cancro de bexiga musculo-invasor (CBMI, estadio >T2) constitui a segunda maior causa de morte entre os tumores geniturinários e variações significativas no prognóstico clinico são observadas para tumores com histopatologia similar devido à heterogeneidade molecular. Mais ainda, tratamentos convencionais baseados em cirurgia e regimes de cisplatina falham em evitar recidivas e disseminação da doença. Assim, a introdução de biomarcadores para a estratificação precisa dos doentes, prognosticação e desenvolvimento de terapia guiada são necessários para melhorar o tratamento destes.

Estudos preliminares do nosso grupo sugerem que tumores de bexiga avançados expressam o antigénio Sialil-Tn (STn) que advém da paragem prematura da O-glicosilação das proteínas da superfície celular. Mais importante ainda, este antigénio não foi detetado no urotélio normal denotando uma natureza cancro-específica. Este antigénio demonstrou ser promotor da motilidade celular, invasão, transição epitelial para mesenquimal e evasão do sistema imune. Em adição, o STn foi encontrado em zonas quiescentes do tumor, sugerindo o seu envolvimento na resistência à quimioterapia.

. Este trabalho demonstrou que a sobre-expressão do STn esteve significativamente associada com tumores de bexiga avançados e sobrevida livre de cancro diminuída independentemente do estadio do tumor. Mais ainda, o STn foi encontrado na metástase de todos os tumores STn positivos. De forma a melhorar a prognosticação do CBMI, a expressão de STn foi incluída no modelo molecular baseado na expressão de queratinas que foi introduzido numa tentativa de reduzir o viés resultante da classificação histopatológica. Conformemente, tumores *basal-like* (KRT14+ e/ou KRT5+ KRT20-) menos diferenciados apresentaram pior sobrevida livre de cancro e sobrevivência livre de doença do que tumores *luminais* ($KRT14^{-}KRT5^{-}$ $KRT20^{+}$) bem diferenciados. A introdução do STn melhorou a capacidade de discriminação deste modelo através da separação de casos com pior sobrevida livre de cancro dentro da população luminal e *basal-like*. No contexto da resposta à quimioterapia, o STn encontrava-se presente na metástase de 70% dos pacientes que progrediram na doença após quimioterapia adjuvante, sugerindo a sua associação com fenótipos quimioresistentes. Suportando estas observações, doentes positivos para STn que foram submetidos a quimioterapia neo-adjuvante mantiveram a mesma

positividade para STn assim como um fenótipo *basal-like* após o tratamento, independentemente do estado de diferenciação inicial do tumor. Para confirmar estes resultados, duas linhas celulares tumorais de bexiga (T24 e HT1376) foram submetidas a tratamento com cisplatina, tendo sido observado que a expressão de STn se mantém inalterada após o tratamento, assim como um enriquecimento no fenótipo *basal-like* entre os clones quimioresistentes. Concomitantemente, uma análise dos transcriptos das células quimioresistentes revelou a activação de programas EMT, associados com a promoção da capacidade de migração e disseminação, assim como programas envolvidos na evasão da apoptose em resposta ao dano no DNA. Em suma, estas observações reforçam a noção de que o STn é um biomarcador de agressividade e quimioresistência e a sua importância no desenvolvimento de terapias guiadas baseadas neste antigénio.

Seguidamente, uma abordagem glicoproteómica foi realizada para identificar glicoproteínas que expressem STn em tumores *basal-like* que conservaram a expressão de STn após quimioterapia neo-adjuvante. Esta abordagem usando nanoLC-ESI-MS/MS permitiu identificar mais de 400 locais O-glicosilados e 143 glicoproteínas de membrana que expressam STn que poderão ser potenciais alvos para terapêutica guiada. Uma das glicoproteínas identificada foi a MUC-16, uma glicoproteína já reportada noutros tumores assim como no soro de doentes com cancro de bexiga, mas não ainda nos tumores de bexiga. Também foram encontradas evidências de alteração da glicosilação no CD44, uma glicoproteína associada ao fenótipo de célula estaminal cancerígena em cancro de bexiga, tendo um papel na mediação da invasão e disseminação da doença. A expressão destas glicoproteínas foi seguidamente validada em tumores primários e na metástase e conservada após quimioterapia neo-adjuvante. Estes resultados não só validam observações anteriores por imunohistoquímica em relação à expressão de STn em tumores de bexiga mas também fornecem um painel de proteínas da superfície celular anormalmente O-glicosiladas que poderão ser usadas para seleccionar tumores de bexiga mais agressivos e melhorar o tratamento da doença. Mais estudos serão necessários para revelar a significância clínica e biológica destas alterações no cancro de bexiga.

Palavras-chave

Cancro de bexiga | Sialil-Tn | Glicosilação de proteínas | Quimioresistência | Células Estaminais Cancerígenas

Abstract

Muscle-invasive Bladder Cancer (MIBC, stage >T2) constitutes the second most common cause of death among genitourinary cancers and significant variations in clinical outcome have been observed for tumors of similar histopathology, due to high molecular heterogeneity. Moreover, conventional treatment relying mostly on surgery and cisplatin-based chemotherapy often fail to avoid disease relapse and dissemination. The introduction of novel biomarkers for accurate patient stratification, prognostication and development of targeted therapeutics is warranted to improve the management of these patients.

Preliminary studies from our group suggest that advanced stage bladder tumors express the Sialyl-Tn antigen (STn), which stems from a premature stop in the O-glycosylation of cell surface proteins. More importantly, the STn antigen was not detected in the healthy urothelium, denoting a disease-specific nature. This antigen was found to impair integrin function, enhance cell motility, invasion and Epithelial to Mesenchymal Transition (EMT), and protect BC cells from host immune responses. Moreover, STn was found in quiescent areas of the tumor suggesting its involvement in resistance to chemotherapy.

This work demonstrated that STn overexpression was significantly associated with advanced bladder tumors and decreased cancer-specific survival (CSS), irrespectively of the stage of the tumor. Furthermore STn was also found in the metastasis of all STn positive tumors. In order to improve MIBC prognostication STn expression was included in a molecular model based on keratin expression, which was introduced in an attempt to reduce the bias resulting from histopathology classification. Accordingly, less differentiated, basal-like tumors (KRT14+ and/or KRT5+ KRT20-) had worse cancer-specific and disease-free survival than well differentiated luminal tumors ($KRT14^{-}KRT5^{-}KRT20^{+}$). The introduction of STn improved the discrimination capability of this model, by sorting cases with worst CSS amongst the luminal and basal-like population. It was also observed that STn was present in the metastasis of 70% of patients that had disease progression after adjuvant chemotherapy, suggesting its association with chemoresistance phenotypes. Also supporting these observations, STn positive patients that underwent neo-adjuvant chemotherapy maintained their STn positivity after treatment and a marked basal phenotype, irrespectively of the initial stage of differentiation of the tumor. To confirm these results, two UC cell lines (T24

and HT1376) were submitted to cisplatin and it was found that STn expression maintained unchanged after two cycles of treatment with cisplatin. Enrichment in basal-like cells was also evident amongst chemoresistant clones. Concomitantly, chemoresistant cell transcripts analysis revealed the activated EMT programs, associated with the enhanced migrating and disseminating capabilities, and the evasion of apoptosis in response to DNA damage. Altogether, these findings reinforce the notion that STn is a biomarker of aggressiveness and chemoresistance and the importance of developing targeted therapeutics based on this antigen.

Then, a glycoproteomic approach was performed to identify altered glycoproteins expressing STn in basal-like tumors that conserved STn expression after neoadjuvant chemotherapy. This glycoproteomic approach using nanoLC-ESI-MS/MS led to the identification of over 400 O-glycosites and 143 membrane STn-expressing glycoproteins that may be potential targets for targeted therapeutics. One of the glycoproteins identified was MUC16, a glycoprotein that has been reported in other tumors as well as in the serum of patients with BC but not yet in bladder tumors. We have also found evidences of altered glycosylation in CD44, a cancer stem cell-associated glycoprotein in bladder cancer, which plays a key role in the mediation of invasion and disease dissemination. The expression of these glycoproteins was further validated in both primary tumors and the metastasis, and found conserved after neoadjuvant chemotherapy. These results not only validate previous observations by immunohistochemistry regarding STn expression in bladder tumors, but also provide a panel of abnormal O-glycosylated cell-surface proteins that may be used to selectively target more aggressive bladder tumors and ultimately improve BC management. More studies are now needed to fully disclose the biological and clinical significance of these alterations in bladder cancer.

Keywords

Bladder Cancer | Sialyl-Tn | Protein Glycosylation | Chemoresistance | Cancer Stem Cells

Index of Contents

Index of Figures

Index of Tables

Abbreviations

67LR 67 kDa laminin receptor

ABC ATP-binding cassette

ALDH1A1 Aldehyde dehydrogenase 1 A1

Asn Asparagine

ATP Adenosine Triphosphate

BC Bladder Cancer

Bcl-2 B-cell lymphoma 2

Bcl-xL B-cell lymphoma-extra large

BCG Bacillus Calmette-Guérin

C1GalT-1 Core 1 β1-3 galactosyltransferase

CD Cluster of Differentiation

CD44v6 CD44 variant 6

CEACAM6 Carcinoembryonic antigen-related cell adhesion molecule 6

CIS Carcinoma *in situ*

cMOAT Canalicular Multispecific Organic Anion Transporter

Cosmc Core 1 Synthase Specific Molecular Chaperone

CSC Cancer Stem Cell

CytC Cytochrome C

DNA Deoxyribonucleic Acid

ECM Extracellular matrix

EMT Epithelial-to-Mesenchymal Transition

ER Endoplasmic Reticulum

ERCC1 Excision Repair Cross-Complementing Group 1 protein

FFPE Formalin-fixed paraffin-embedded

Fuc-TIII alpha1,3/4fucosyltransferase

Fuc-TVIII alpha-(1,6)-fucosyltransferase

GA Golgi Apparatus

GalNAc N-acetylgalactosamine

GlcNAc N-acetylglucosamine

GnT-III β1,4 N-acetylglucosaminyltransferase III

GnT-V β1,6 N-acetylglucosaminyltransferase V

GSH Glutathione

GST Glutathione S-transferase

HCC Hepatocellular Carcinoma

HDAC4 Histone Deacetylase 4

hMLH1/2 human mutL homolog 1/2

IAP Inhibitor of Apoptosis family of proteins

KRT5/14/17/20 Keratins 5/14/17/20

MDR1 Multidrug Resistance Gene 1

MET Mesenchymal-to-Epithelial Transition

MIBC Muscle Invasive Bladder Cancer

MMR Mismatch Repair System

MRP1/2/4 Multidrug Resistance-associated Protein 1/2/4

MT Metallothioneins

MUC1 Mucin 1 Protein

MVAC Chemotherapy Regimen of Methotrexate, Vinblastine, Adriamycin and Cisplatin

NER Nucleotide Excision Repair System

NMIBC Non-Muscle Invasion Bladder Cancer

PBS Phosphate Buffered Saline

P-gp P-glycoprotein

ppGalNAcT Polypeptide N-acetylgalactosamine transferase

SCC Squamous Cell Carcinoma

Ser Serine

Sia6LacNAc α2,6-sialylated lactosamine

SIRPα Signal Regulatory Protein

Smac/DIABLO Second Mitochondria-derived Activator of Caspase/Direct Inhibitor of Apoptosis-binding Protein with low pI

SP Side Population

ST6Gal-I β-galactoside α2,6-sialyltransferase-I

ST3GalNAc-I/III β-galactoside α2,3-sialyltransferase-I/III

ST6GalNAc-I/VI Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase I/VI

STn Sialyl Tn

T antigen Thomsen-Friedenreich antigen

Thr Threonine

TNF Tumor Necrosis Factor

TP53 Tumor Protein 53

TRAIL TNF related apoptosis inducing ligand

TUR Transurethral Resection

UCC Urothelial Cell Carcinoma

UDPGalNAc Uridine diphosphate –N-acetylgalactosamine

VEGFR2 Vascular Endothelial Growth Factor Receptor 2

XIAP X-linked Inhibitor of Apoptosis Protein

XPC Xeroderma Pigmentosum group C protein

XPF Xeroderma Pigmentosum complementation group C protein

Chapter I | Introduction

1. Bladder Cancer

1.1. Bladder Cancer epidemiology and risk factors

Bladder cancer (BC) is the most common malignancy of the urinary tract and the ninth most common cancer worldwide with 380 000 new cases and 150 000 deaths per year [1]. In Portugal, BC is the eighth most common cancer and it is estimated about 3000 cases and 900 deaths in 2015. The disease is more common in men than in women (male:female ratio is 3:1) and the medium age at diagnosis is 70 years [2]. However, women present advanced stages of the disease and have less favorable prognosis [3].

Environmental risk factors associated with BC include tobacco smoke, consumption of arsenic-contaminated water, exposure to aromatic amines and polycyclic hidrocarbons, chronic infection with *Schistosoma spp*, exposure to ionizing radiation and also genetic factors namely N-acetyltransferase 1 (NAT1), N-acetyltransferase 2 (NAT2) and glutathione S-transferase µ1 (GSTM1) polymorphisms [4]. Tobacco smoke is the most common risk factor associated with BC with about 50% of BC cases attributed to smoking [5].

Haematuria is the most common symptom seen in approximately 80% of patients. Other symptoms include urgency, dysuria, pelvic pain and symptoms related to urinary tract obstruction [6].

1.2. Diagnosis, Pathophysiology and Treatment of BC

Clinical diagnosis of BC is based on cystoscopy and urine cytology. Cystoscopy is effective for detecting papillary tumors while urine cytology is specific to detect high-grade tumors or carcinoma *in situ* (CIS). CIS is diagnosed by a combination of cystoscopy, urine cytology, and histologic evaluation of multiple bladder biopsies [7].

Bladder cancer arises from transitional cells of the bladder mucosal epithelium in 90% of cases (urothelial cell carcinoma, UCC). Other histological types include squamous cell carcinoma (SCC) and adenocarcinoma [7]. For instance, in places

where the incidence of schistosomiasis is high, SCC is the most frequent type and BC may be the most common cancer. The dual tract concept of human bladder carcinogenesis postulates two distinct but overlapping pathways of urothelial carcinoma pathogenesis: the papillary and non-papillary pathways. Exophytiic papillary tumors arise from hyperplasia and minimal dysplasia of a preneoplastic clone protruding the mucosal surface, present loss of heterozygosity of chromosome 9 and harbor mutations in Fibroblast Growth Factor Receptor 3 (FGFR3), Harvey rat sarcoma viral oncogene homolog (HRAS), Phosphoinositide-3-kinase (PIK3CA) and Stromal Antigen 2 (STAG2) genes. These superficial tumors frequently recur (~75%) but infrequently progress (10%) to muscle invasive disease which presents a less favorable prognosis. Non-papillary invasive tumors invade the muscle wall and adjacent organs and are thought to arise from flat dysplasia and CIS. These tumors may present genetic instability with frequent loss of tumor suppressors Retinoblastoma 1 (RB1) and tumor suppressor protein p53 (TP53) in addition to chromosome 9 deletions [3]. Despite the non-invasive nature of CIS, it has a poorer prognosis than other superficial tumors.

Most of diagnosed bladder cancer cases (~80%) are superficial or non-muscle invasive bladder carcinomas (NMIBC). The stage and grade of superficial tumors include low-grade papillary tumors confined to the mucosa (Ta), high-grade flat lesions or *CIS* and high-grade papillary tumors invading the subepithelial connective tissue (T1). The standard treatment of NMIBC is complete transurethral resection (TUR) followed by a schedule of intravesical instillations with attenuated strains of *Mycobacterium bovis* (the *Bacillus Calmette-Guérin,* BCG) for high-risk of recurrence/progression tumors. This procedure promotes a strong immunological response that contributes to eliminate the residual tumor. However, one third of the patients present intolerance to BCG immunotherapy and may present progression to the muscle invasive disease. The remaining 20% of cases are muscle-invasive bladder cancers (MIBC) that include tumors that invade superficial muscle (stage T2a), deep muscle (T2b), perivesical tissue (T3) and adjacent tissues and organs (T4) (Fig.1). These tumors are treated by radical cystectomy with extended lymphadenectomy and are also submitted to neo-adjuvant or adjuvant cisplatin-based chemotherapy, before or after cystectomy respectively, in order to reduce the risk of metastasis. Five-year survival for patients in this group is 50% and about 50% of patients develop metastatic disease within five years [8].

At the present, there exist a lack of specific biomarkers that target aggressive cell phenotypes. Additionally, molecular heterogeneity within invasive tumors is such that remains difficult to stratify patients into those facing worst prognosis as well as

predict MIBC response to chemotherapy based only in histological approaches. The identification of those biomarkers would possibly prevent radical cystectomy as well as reduce the chance of poor outcome. Moreover, due to the long-term follow-up and the repeated treatment of recurrent disease, BC is the costliest to treat among solid tumors therefore urging the introduction of novel biomarker panels [9].

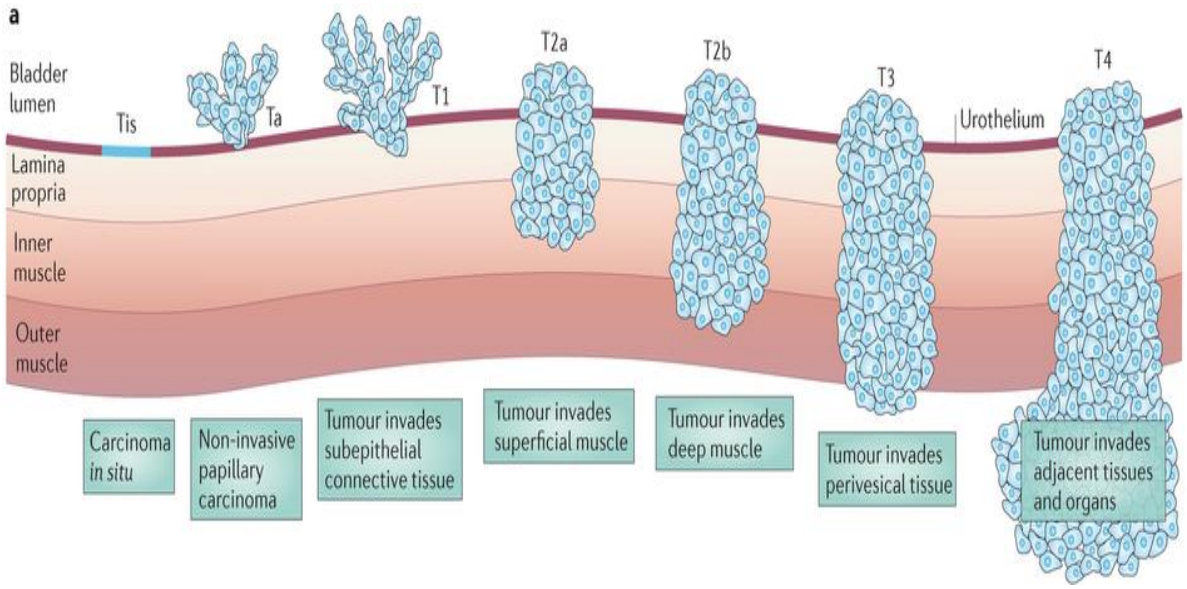


Figure 1 | Bladder cancer staging according to the Tumor Node Metastasis System (TNS) [3]. The stage of the primary tumor (T) is based on the extent of penetration or invasion into the bladder wall.Tis, Tumor in situ: ‘‘flat tumor’’; Ta, Non-invasive papillary carcinoma; T1, Tumor invades subepithelial connective tissue; T2, Tumor invades muscle; T2a, Tumor invades superficial muscle (inner half); T2b, Tumor invades deep muscle (outer half); T3, Tumor invades perivesical tissue; T4, Tumor invades any of the following: prostate, uterus, vagina, pelvic or abdominal wall.

Recently, studies from our group pointed out that high-grade NMIBC and MIBC express the Sialyl-Tn antigen (STn). This cancer-associated glycan results from the premature stop in the O-glycosylation of cell-surface proteins. This antigen was not found in the healthy urothelium and its presence was correlated with migration and invasion *in vitro*. Moreover, STn expression was found in non-proliferative areas of the tumor, recognized as sites with high capacity in overcoming chemotherapeutic treatments [10]. Nevertheless, more exploratory data is needed to better evaluate STn as a diagnostic and therapeutic biomarker. As such, the identification of the proteins carrying STn would be a step forward in order to achieve a relation between its appearance and the dysregulations normally present in BC cells. If so, guided therapeutics that specifically target STn positive cells could provide a complementary therapy against this aggressive chemoresistant cells.

2. Chemoresistance mechanisms and Cancer Stem Cells selection in Bladder Cancer

Anticancer drugs such as cisplatin-based regimens are extensively used in cancer treatment. However, its failure is recurrent in cancer patients making this approach not fully effective. In spite of being part of most therapeutic schemes for solid tumors such as BC, low response rates are obtained using chemotherapy drugs. A major cause of resistance is the development of drug resistance mechanisms against these agents. In the BC case, changes in intracellular cisplatin concentration, alterations of DNA repairing systems and changes in apoptosis regulatory pathways are the most described mechanisms. Recent data also suggests that chemotherapy can act as a selective pressure in order to maintain a pool of chemoresistant cancer cells with stem characteristics (cancer stem cells, CSCs) capable of recapitulating tumor heterogeneity. Furthermore, these cells might present epithelial-to-mesenchymal transition (EMT) phenotypes, responsible by endowing them with the capability to invade, disseminate and colonize distant locations [11]. Thus, this evidences mentioned above explain the failure to prevent tumor relapse and disease dissemination after chemotherapy treatment. Focusing attention on these considerations, the following sections are aimed to explore chemoresistance mechanisms in BC, CSCs and the association between chemoresistant bladder CSCs and EMT.

2.1. Mechanisms of chemoresistance in Bladder Cancer

2.1.1. Changes in intracellular cisplatin concentration

There are at least two described ways by which cancer cells provide cisplatin resistance: a reduced intracellular concentration of cisplatin and an increased sequestration of this agent by cellular scavengers with nucleophilic properties.

In spite of the fact that cisplatin efflux is manly mediated by two copper extruding P-type Adenosine Triphosphatases, ATP7A and ATP7B, the canalicular multispecific organic anion transporter (cMOAT)/Multidrug Resistance-associated Protein 2 (MRP2) seems to be the upregulated in cisplatin-resistant cell lines [12] and may also play a role in the modulation of cisplatin resistance in BC. As such, cMOAT was shown to be upregulated in the T24 UCC cell line, where its expression correlated with decreased cisplatin accumulation [13]. Despite this factor, further studies involving cMOAT expression and cisplatin resistance had not involved BC cell lines [14]. Likewise, it seems that chemotherapy induces the transactivation of the Multidrug Resistant gene 1 (MDR1) that encodes the P-glycoprotein (Pgp), an energy-dependent efflux pump [15]. Moreover, high MDR1 gene expression correlated with inferior survival in patients with locally advanced BC receiving adjuvant chemotherapy [16].

Even tough cisplatin exerts its function in the N7 of purine atoms in DNA, a substantial majority of DNA molecules react with other ligands before entering in the nucleus. Cisplatin exhibit higher affinity to sulfur donors than nitrogen donors, therefore detoxification by intracellular thiols such as metallothioneins (MT), glutathione and thioredoxin represent the main mechanisms of cisplatin scavenging in BC. As such, cisplatin resistance has been correlated with the overexpression of MT, a class of low-molecular weight cysteine-rich proteins that promote heavy metal detoxification and protect cells against oxidative stress [17]. This finding was observed in BC cell lines [18] as well as *ex vivo* where bladder tumors with low levels of MT had a tendency to respond better to cisplatin chemotherapy [19]. Moreover, BC mouse xerographs have also been sensitized to cisplatin following propargylglycine treatment, an inhibitor of MT synthesis [20]. Altogether, these evidences reinforce a correlation between overexpression of MT and poor outcome after chemotherapy.

Glutathione (GSH) is a tripeptide that plays an important function in the detoxification of xenobiotic substances by scavenging free radicals. GSH and cisplatin can form GSH-cisplatin conjugates, a process catalyzed by glutathione S-transferases (GST), particularly GSTP1-1. In addition, GSH and cMOAT/MRP2 work together in order to pump GSH-cisplatin conjugates out of the cells in an ATP-dependent manner) [21]. A correlation between cisplatin resistance and expression of the glutathione system has been extensively reported in many cancer cell lines such as ovarian or lung, [22] as well as in BC cell lines. In the BC case, high levels of GSH and GST were seen in the less sensitive cells suggesting a role of glutathione in mediating cisplatin resistance [23]. Additionally, buthionine sulphoximine (BSO) and indomethacin which deplete GSH and GST respectively significantly decreased cisplatin resistance in T24

bladder cancer cells. These observations support the notion that glutathione-mediated detoxification is involved in cisplatin resistance in bladder cancer cell lines [24].

Thioredoxin has also been associated with cisplatin resistance in BC cell lines. Levels of this redox protein and mRNA were higher in cisplatin-resistant derivatives of RT112 and KK47 cell lines and in cells where thioredoxin expression was reduced, cisplatin sensitivity was higher [25].

2.1.2. Alterations in DNA repairing systems

The contribution of DNA repair for cisplatin resistance has been shown in many cancer types and increased ability to repair damaged DNA has been associated with cisplatin resistance in BC. The Nucleotide Excision Repair (NER) system deals with bulky adducts that cause a distortion of the DNA *helix* and intra/inter-strand cross-links induced by DNA-damaging or cross-linking agents. Cisplatin adducts are able to distort DNA [26] therefore causing the recruitment of NER-associated proteins. The NER pathway is commonly split into DNA damage recognition, DNA unwinding and DNA incision however is in the incision-mediated proteins that reside most of the attention in relation to cisplatin resistance in BC most particularly in the ERCC1/XPF complex. *Bellmunt et al.* examined ERCC1 expression in formalin-fixed, paraffin-embedded surgical specimens from advanced and metastatic BC patients treated with cisplatin-based regimens and found a relation between low ERCC1 expression levels and increased overall survival in these patients [27]. Moreover, *Kavashima et al.* found out ERCC1 expression in four BC cell lines, including two cisplatin-resistant and concluded that ERCC1 expression was higher in the resistant cell lines. Despite this, ERCC1 siRNA did not led to a significant increase in cisplatin sensitivity [28]. Finally, *Usanova et al.* observed that ERCC1-XPF downregulation in one BC cell line correlated with a slightly but significantly increase in sensitivity to cisplatin [29]. Altogether, these observations support that ERCC1 might play a role in the resistance to cisplatin in BC.

XPC, another NER-associated protein involved in the recognition of DNA-cisplatin adducts and a key intermediate in cell cycle checkpoint control and apoptosis, is commonly found downregulated in BC cell lines and in tumors where it is associated with cisplatin resistance [30]. Emerging evidences suggests HDAC4 as a candidate in XPC downregulation and increase levels of HDAC4 in bladder tumors correlated with increase cancer severity [31]. These facts strongly suggest XPC as a critical partner in preventing BC progression.

The Mismatch Repair (MMR) system is another common DNA repairing system that recognizes cisplatin-induced DNA damage particularly base-base mismatches and insertion-deletion loops. Downregulation of MMR proteins, particularly hMLH1, has been correlated with cisplatin resistance in many tumor types. Little is known about this correlation in BC however reduced hMLH1 and hMLH2 have been found in advanced bladder tumors whereby this might be a future area of interest in BC [32].

2.1.3. Changes in apoptosis regulatory pathways

Cisplatin exerts its cytotoxic effects through the initiation of apoptotic pathways in response to the impossibility to repair DNA damage. The apoptotic cascade has been subclassified into two types, the intrinsic pathway and the extrinsic pathway. The first involves the mitochondria and the transduction of upstream signals mediated by anti or pro-apoptotic proteins. This culminates in the release of cytochrome C (CytC) leading to the activation of initiator caspases following to effector caspases. The extrinsic pathway provides the transduction of extracellular signals such the presence of “death ligands” and the activation of initiator and effector caspases. Fail in the apoptotic cascade has been correlated with cisplatin resistance in BC cell lines as well as in clinical samples). Moreover, dysfunction of p53 signaling pathways have also been linked with cisplatin resistance in BC [33]. As such, apoptosis-related proteins may represent a good target for therapeutic intervention.

Among the intrinsic pathway, the anti-apoptotic members of the Bcl-2 family of proteins Bcl-2 and Bcl-X_L have been shown to be upregulated in cisplatin-resistant BC cell lines and attenuation of this overexpression restored cisplatin sensitivity [34, 35]. In line with this observation, a study carried out in the T24 cell line and in a cisplatin-resistant sub-line showed high levels of Bax and CytC after cisplatin exposure in the parental cell line. Conversely, Bcl-2 expression was increased in the resistant cell line thus inhibiting Bax translocation to the mitochondrial membrane resulting in reduced cell death [36]. Moreover, *Miyake et al.* transfected the BC cell line KoTTC-1 with an expression plasmid containing the Bcl-2 gene and observed that this conferred resistance to cisplatin and decreased apoptosis after cisplatin treatment. Additionally, cells overexpressing Bcl-2 were then injected subcutaneously into mice resulting in less cisplatin response and inferior prognosis when compared with control xenographs [37]. Expression levels of the Bcl-2 protein were also seen in BC clinical samples as Cooke et al. observed in a cohort of 51 patients who received neo-adjuvant cisplatin chemotherapy that Bcl-2 negative tumors had a significantly better prognosis [38].

Furthermore Bfl-1, another Bcl-2 family member, has also been shown to be upregulated via NF-kB activation in a cisplatin-resistant BC cell line where it increases cisplatin resistance [39].

The inhibitor of apoptosis (IAP) member XIAP may also play a role in cisplatin resistance in BC cells. XIAP binds to the mitochondrial protein Smac/DIABLO which displaces XIAP from caspase 9 therefore promoting apoptosis. Preliminary experiments demonstrated that high XIAP and low Smac/DIABLO levels correlated with high stage and high grade bladder tumors. *Bilim et al.* reported considerable XIAP levels in four cisplatin-resistant cell lines [40]. High mRNA levels of the XIAP inhibitor XAF-1 were found in bladder cancer patients with a more favorable clinical outcome after cisplatin-based chemotherapy [41]. Moreover, cisplatin-resistant BC cell lines have been shown to present low levels of Smac/DIABLO expression when compared with the parental cell line thus suggesting a contribution in cisplatin resistance [42].In vivo experiments in BC xenographs have demonstrated that treatment with the Smac mimetic AZ58 alone or in combination with cisplatin-based regimens resulted in increased apoptosis and decreased cellular proliferation [43]. Survivin, another member of the IAP family has been also shown to be upregulated in the T24l cell line [44] as well as in tumor material where its expression correlated with clinical poor outcome [45]. According to these factors, strategies targeting XIAP, Smac/DIABLO and Survivin can be useful to overcome cisplatin resistance in BC.

Dysregulations in proteins involved in the extrinsic pathway have also been linked with cisplatin resistance in BC. Ligands capable of initiating the extrinsic pathway (or “death ligands”) such as CD95L (or Fas Ligand), TNF related apoptosis inducing ligand (TRAIL) and their receptors are among the targets in BC cancer therapy. Treatment of BC resistant cell lines with either TRAIL or CD95L showed a significant increase in the cytotoxicity mediated by cisplatin [46, 47]. Recent work using human agonistic antibodies that induce apoptosis by targeting the TRAIL Receptor 2 (TRAILR2) such as *lexatumumab* demonstrated a synergistic effect between *lexatumumab* and cisplatin in the T24 cell line [48]. In spite of this factor, no similar experiences were made in cisplatin-resistant BC cell lines. Furthermore, cellular FLICE (FADD-like IL-1β-converting enzyme)-Inhibitory Protein (c-FLIP), a protein that negatively regulates the signaling complex downstream of death receptors seems to be an important player in cisplatin resistance in BC cells. Suppression of c-FLIP expression by siRNA in the T24 resistant cell line T24R2 rendered cells more sensitive to cisplatin when compared with the untransfected T24R2 [49].

The tumor suppressor protein p53 is activated in cancer cells after treatment with chemotherapeutic drugs inducing both cell cycle arrest and apoptosis [50].

Sensitivity to cisplatin correlates positively with the presence of the wild-type p53 in a panel of cancer cell lines [51] as well as in BC cell lines [33]. Despite tumor cell lines lacking functional p53 are more resistant to cisplatin than cells that carry a functional p53, sensitivity to cisplatin could be restored upon reconstitution with the proficient p53 protein in these cell lines [52, 53] In the BC case, adenovirus-mediated overexpression of wild-type p53 in resistant cell lines has been shown to increase cell cycle arrest and apoptosis when compared to the parental counterparts and also increase in p53-mediated expression of p21 and Bax [54]. In spite of this, other studies in BC revealed conflicting findings on whether p53 mutations confer resistance or responsiveness to cisplatin-based chemotherapy [55]. *Cote et al*. reported that BC patients that benefited from MVAC chemotherapy were those with p53 alterations [56]. Moreover, Qureshi et al. reported that p53 immunoreactivity could not be used to predict tumor response and patient survival in a cohort of patients with invasive BC [57]. Altogether the above mentioned evidences reinforce the controversy in considering p53 alterations as a predictive factor for prognosis and chemosensitivity.

2.2. Bladder Cancer Stem Cells

Overall, there is a growing amount of data supporting the role of cisplatin in the enrichment of a chemoresistant pool of cells named cancer stem cells (CSC) in many tumor types [11, 58-60] including BC [61, 62]. In spite of sharing many properties with normal stem cells such as self-renewal and asymmetric differentiation capacity, slow cycling, high proliferation upon passage, clonogenic capacity and phenotypic plasticity, CSCs differ from these cells as well as from cells of the tumor bulk, the basic concepts of the CSC hypothesis. This notion is based on the fact that not all the cells within the tumor have equal capacities for tumorigenesis, recurrence and metastasis, common features of CSCs. As such, CSCs are the subpopulation responsible for initiate, sustain and expand disease. All of these concepts have been confirmed by xenograph experiments using many cancer types and cell lines [63, 64].

Since the discovery of the existence of CSCs in leukemia that many questions have been made about the origin of these cells. Within the bladder urothelium, there are three layers composed of cells with different differentiation levels, the basal, the intermediate and the superficial layers. The degree of differentiation increases from the basal lining the *lamina propria* to the superficial layer adjacent to the lumen of the bladder. In fact, evidences support the hypothesis that a small portion of the basal cell layer contains urothelial stem cells and that these are the precursors of the transit-

amplifying cells in the intermediate layer and the umbrella cells in the superficial one [65]. Kurzrock and colleagues identified a slow-cycling population of cells in the rat bladder which retained the the bromodeoxyuridine label in their DNA. This “label retaining cells” (LRC) demonstrate infrequent proliferation and long lifespan, characteristics of stem cells. Moreover, these cells reside in the basal layer and present greater clonogenic capacity than the unlabeled cells, confirming that stem cells may reside in the basal compartment [66]. It´s currently believed that BC arises from a CSC derived from the transformation of a normal basal cell progenitor [67]. As such, mutations in the cell of origin, epigenetic modifications and tumor-stroma interactions might favor CSC arising. However the CSC origin in BC is still under debate as recent evidences showed that umbrella cells can develop independently of the basal cell layer cells [68]. Moreover, CSCs had only been identified in muscle invasive tumors, raising the hypothesis that not all BC derive from a common progenitor [67, 69-71]. As a matter of fact, current data indicates that the papillary or non-invasive bladder tumors may derive from a non-basal cell while invasive tumors may derive from a basal cell progenitor [72]. In spite of these statements, the question of the urothelial cancer cell of origin is not a finished subject.

In order to prove that a subpopulation of cells is in fact a CSC subpopulation, many approaches have been made to isolate and identify these cells. The growth of spherical colonies in serial passages, the generation of a mix of undifferentiated and differentiated cells and the upregulation of self-renewal transcription factors such as Nanog, Oct-4 and Sox-2 are considered to indicate self-renewal capacity. Moreover, the “side population” (SP) functional assay is also used to isolate CSCs. The overexpression of ATP-binding cassette (ABC) transporters and multidrug resistance pumps that are able to pump out DNA-binding dyes such as Hoechst 33342 or the DyeCycle Violet is a common characteristic of CSCs and the basic science of the SP assay. Efflux of these dyes defines a side population that is enriched for CSCs and can be detected using Fluorescence-activated cell sorting (FACS). All of these *in vitro* approaches are always followed by xenotransplantation of cells into immunocompromised mice and its ability to induce tumorigenesis *in vivo* in order to confirm the CSC phenotype of the isolated cell population. *She and colleagues* showed that SP cells isolated from BC cell lines exhibited greater clonogenic and self-renewal capacity and can initiate tumors when injected into immunocompromised mice. Furthermore, the expression of ABC transporters and self-renewal transcription factors also sustained the stem-cell phenotype of the SP cells [71]

To efficiently treat cancer, molecular-based therapy that target CSC in combination with therapies that target the bulk of the tumor would be a step forward

[73, 74]. CSCs reside in niches that are difficult to a reach by chemotherapeutic agents. In BC there are several cell-surface and intracellular potential markers that would possibly be used to clearly identify CSCs which might be useful for diagnostic purposes. CD44 is one of these markers as it has been reported by Chan and colleagues. This cell- surface glycoprotein has been found in the basal layer of the urothelium and has the ability of isolating CSC in muscle invasive bladder tumors. Moreover, the $CD44^+$ population showed a tumorigenic potential of at least twenty fold higher than the $CD44^-$ population as well as a mixture of well-differentiated and less-differentiated cells when the same comparison was made. Further characterization found that CD44 expression co-localizes with the expression of the basal cell marker cytokeratin 5 (KRT5) and not with the superficial cell marker cytokeratin 20 (KRT20) sustaining the hypothesis of the basal-like property of CSCs. Additionally, it was found out in BC tissues that the isolated $CD44^+$ population exhibited a highly-expressed group of genes when compared to the $CD44^-$ counterparts, the so called bladder tumor-initiating cell gene signature. These genes were also found upregulated in the majority of muscle invasive tumors but downregulated in most non-invasive forms of the disease. Among non-invasive tumors, the time to recurrence to the invasive form was shorter in the ones that displayed an activated tumor-initiating cell gene signature. This gene signature could be an important prognostic marker in the identification of patients with non-invasive BC at risk of progression to the invasive form. In spite of all of these statements, it was found a negative staining for CD44 in a wide array of BC tissues and that $CD44^-$ primary patient tumors also engrafted when xenotransplanted in immunocompromised mice which might indicate that CD44 is not a general marker for all bladder CSCs and sustains the hypothesis of other origins for CSCs [69].

Other studies demonstrated that $CD44v6^+MUC1^-$ and $KRT17^+67LR^+$-$CEACAM6^-$ as subpopulations that are enriched in CSCs. *Yang et al.* showed in BC specimens that the $MUC1^-$ and the $CD44v6^+$ subset of cells exhibited greater clonogenic capacity than the unselected cells and are located in the basal cell layer of the urothelium [75]. However, a study revealing a link between the absence of CD44v6 and an increase in recurrence risk and worse survival rate seem to contradict these results [76]. In turn *He et al.* demonstrated in xenographs formed from the SW480 cell line that the $67LR^+$ subpopulation is at least 10-fold enriched in tumorigenic cells and the $CEACAM6^-$ subset of cells is 70-fold enriched for tumorigenic potential. The authors also found that the basal cell marker cytokeratin 17 (KRT17) co localizes with 67LR positive tumor cells but is mutually exclusive to CEACAM6. Moreover, the gene expression profile of the highly tumorigenic $67LR^+$ cells revealed an increase in genes involved in chemoresistance as well as in genes associated with the Wnt signaling pathways when

compared with the 67LR$^-$ cells. Overall, these evidences reinforce the tumor-initiating potency of the basal-like cells [67].

CD133 and CD47 cell-surface glycoproteins are also considered as potential markers of cancer stemness. In a study conducted by *Huang et al.* CD133$^+$ cells of the human BC cell line J82 tended to colonize animal models during their growth when compared with the CD133$^-$ pool. Moreover, upregulation of the pluripotent stem cell factors Sox-2 and Oct-4 and an increased tolerance to cisplatin and BCG were also seen in CD133 positive cells. *In vivo* assays confirmed the previous data as CD133+ cells demonstrated greater tumorigenic potential than the CD133$^-$ counterparts [77]. Regarding CD47, this glycoprotein was found expressed on all BC cells but significantly higher on the CD44+ CSCs. CD47 interacts with SIRPα in cells such as macrophages and dendritic cells thus inhibiting phagocytosis. Blockade of CD47 with a monoclonal antibody resulted in efficient phagocytosis and elimination of human BC cells. Despite the lack of *in vivo* experiments using anti-CD47 antibodies, targeting CD47 might be a promising strategy in bladder cancer therapy [69]

Recently, it has been reported that a cell population with high activity of the intracellular protein aldehyde dehydrogenase 1 A1 (ALDH1A1) is also enriched in CSCs. ALDH1A1$^+$ cells of the BC cell lines HTB-2, HTB-4 and HTB-9 showed an increased clonogenic capacity *in vitro* and 100-fold increased tumorigenic potential *in vivo* when compared with ALDH1A1$^-$ cells. Furthermore high ALDH1A1 expression was directly correlated with advanced pathological stage, high histological grade, recurrence and metastasis and inversely associated with cancer-specificity and overall survival [78]. Many other markers such as VEGFR2 [79], CD177 [79], Nestin [80] and the ABC family transporters [79, 81] seem to be present in CSCs. In spite of the existence of many functionally distinct subsets of CSCs based on the expression of several markers, the relationship between these CSC populations is still unclear.

In addition to the ability of recapitulating tumor heterogeneity, CSC may also undergo EMT and Mesenchymal-to-epithelial transition (MET), considering the most important driving forces in cancer dissemination. The term Epithelial to-Mesenchymal transition (EMT) refers to a process by which epithelial cells reprogram and acquire mesenchymal traits such as motility and invasive properties in response to a defined set of extracellular stimuli. Epithelial cells form tight homotypic junctions that function as a permeability barrier. The most important cell-to-cell adhesion molecule is E-cadherin and its interaction with β-catenin and the actin cytoskeleton plays an important role in promoting the connections between adjacent epithelial cells. However, when EMT is activated E-cadherin expression is replaced by N- and P-cadherin expression, the so called “cadherin switch”. This switch and downregulation of E-

cadherin is associated with release of β-catenin which migrates to the nucleus and induce expression of EMT-inducing transcription factors. The EMT is also controlled by by a group of transcriptional repressors such as ZEB-1, ZEB-2, TWIST, Snail and Slug as well as microRNA-200 family members (miR-200). These transcriptional repressors bind to the E-boxes of the promoter of the E-cadherin-encoding gene (CDH1) therefore resulting in CDH1 repression. In turn, miR-200 family members appear to be involved in EMT as the loss of its expression result in the accumulation of ZEB-1 and ZEB-2 thereby promoting EMT and tumor invasion. Other hallmarks of EMT include the activation of Rac/Rho/Cdc42 GTPase family involved in cytoskeleton reorganization and the increase of matrix metalloproteinases (MMPs) that proteolytically degrade various components of the extracellular matrix (ECM).

The EMT is strongly associated with recurrence, progression, metastasis and poor overall survival in BC [82-84]. Moreover, EMT programs seem to be activated in bladder CSCs suggesting that the induction of EMT can induce stem cell properties [61] as described by other authors in other tumor types [85-87]. Despite the lack of information about the molecular mechanisms underlying EMT and MET in the generation of bladder CSCs, these concepts were integrated by Brabletz and colleagues using colorectal cancer as a model [88]. These authors proposed the existence of two types of CSCs, the stationary CSCs (SCSC) and the migrating CSCs (MCSC). Tumor microenvironment might secrete EMT-inducing factors that provide the switch of SCSCs to MCSCs which might be the trigger for dissemination and metastasis. Moreover this proposal could also explain MET at distant sites where cells need to change to an epithelial phenotype in order to adhere to their surroundings. At distant sites, the microenvironment might not secrete EMT-inducing signals therefore undergo MET [88]. These concepts would possibly connect CSCs and EMT in BC however, molecular mechanisms underlying EMT and MET in the generation of bladder CSCs are still under debate.

3. Protein Glycosylation in cancer

3.1. Altered patterns of protein glycosylation in cancer

Protein glycosylation is the most frequent posttranslational modification that occurs within proteins and results from an enzymatic linkage of monosaccharides or even whole oligosaccharides to specific amino acids. This process involves many glycosyltransferases and glycosylases using specific sugar donor substrates in the endoplasmic reticulum (ER) and in the Golgi apparatus (GA) in order to generate carbohydrate-associated proteins. Glycans play many biological roles such as mediators of cell-to-cell adhesion, immune recognition and host-pathogen interactions, protein folding and cell signaling pathways. There are at least five types of glycosylation in glycoproteins, O-glycosylation, N-glycosylation, C-mannosylation, Phosphoglycosylation and Glypiation; however O- and N-glycosylation are the most commonly detected types found at the cell-surface. N-glycosylation occurs co-translationally during the translation and transport of proteins into the ER and is based on the addition of an oligosaccharide to an Asparagine (Asn) residue in the sequence context Asn-X-Serine (Ser)/Threonine (Thr) where X can be any amino acid except proline (Pro). This process is initiated in the cytosolic surface of the ER membrane by addition of a precursor glycan (Glc3Man9GlcNac2-) from dolichol pyrophosphate to the Asn residues of nascent polypeptide chains. When the glycoprotein has normally folded and reached the GA, then a sequence of both trimming and adding sugars occur in the growing chains giving rise to a wide range of N-glycans. In turn, O-glycosylation, which also takes place initially in the GA, occurs post-translationally and consists in the transfer of monosaccharides to the –OH of Ser or Thr (in a lesser extent hydroxiproline and hydroxilysine) within proteins. The most ubiquitous type of O-glycosylation is the O-GalNAc one, often called mucin-type O-glycosylation, due to the high content of VNTR motifs found in mucins carrying clusters of α-N-acetylgalactosamine (GalNAc)-based glycans in its Ser/Thr residues. This process consists in the transfer of GalNAc from the donor-nucleotide sugar uridine diphosphate –N-acetylgalactosamine (UDP-GalNAc) to one of the above referred amino acids. This initial reaction forms the Tn antigen and is catalyzed by the enzyme family UDPGalNAc-polypeptide-N-acetyl-galactosaminyltransferase (ppGalNAcT). Subsequently, with the addition of the next sugar, core structures are synthesized. Core 1 (or T antigen) arises from the

attachment of a galactose to the GalNac structure, a process catalyzed by the core 1 β1-3 galactosyltransferase (C1GalT-1) termed T synthase. In order to be exported from the ER and to display its full activity in the GA, T synthase binds to the molecular chaperone Cosmc preventing its proteosomal degradation. Lack of Core 1 synthesis can be attributed to defective T synthase or the absence of functional Cosmc [89]. There are eight core structures which can be further substituted by other sugars. Mature O- and N-glycans may present similar terminal structures such as sialic acids, Lewis (Le) blood group related antigens or ABO(H) blood group determinants.

Several other types of non-mucin O-glycans exist within glycoproteins including α-linked O-fucose, β-linked O-xylose, α-linked O-mannose, β-linked O-GlcNAc (*N*-acetylglucosamine), α- or β-linked O-galactose, and α- or β-linked O-glucose glycans. Particularly, O-glycosylation of the O-GlcNAc type was found in intracellular proteins, a notion firstly demonstrated by Torres and Hart [90]. O-GlcNAcylation competes with phosphorylation for Ser and Thr resides and may function as a nutrient sensor enabling the cell to adapt the presence of low, normal or high glucose levels. Since the discovery of intracellular O-GlcNAcylation that many proteins have been found to be regulated by this posttranslational mechanism, namely transcription factors [91].

In cancer tissues, glycosylation patterns are profoundly altered and in some cases recapitulate the antigens expressed during fetal life [92]. Aberrant glycan structures are highly specific which increases molecular heterogeneity within glycoproteins. Moreover, different mechanisms are associated with the shift in the glycosylation patterns observed in cancer cells. These include alterations in the expression of glycosyltransferases, sugar and sugar-nucleotide transporters and glycosidases, competition within glycosyltransferases for the same substrate and masking of sugar structures by other groups. In relation to the cancer-associated changes in glycosylation, the most relevant modifications are *O*-glycan truncation, sialylation, fucosylation and β1,6 branching of N-linked chains. These changes are the next topic of analysis.

3.1.1. O-glycan truncation

Truncated O-glycans stem from the premature stop in the O-glycosylation of proteins [93]. Examples of these truncated structures are the Tn antigen, its sialylated counterpart sialyl-Tn (STn, Neu5Acα2-6GalNAcα-*O*-R) and the T antigen (Fig.2). These antigens have been found overexpressed in different carcinomas such as gastrointestinal [94-96], breast [97], pancreas [98] and ovary [99] cancers. Additionally,

these antigens are either absent or only weakly expressed in normal tissues which makes them ideal targets for both diagnosis and therapy.

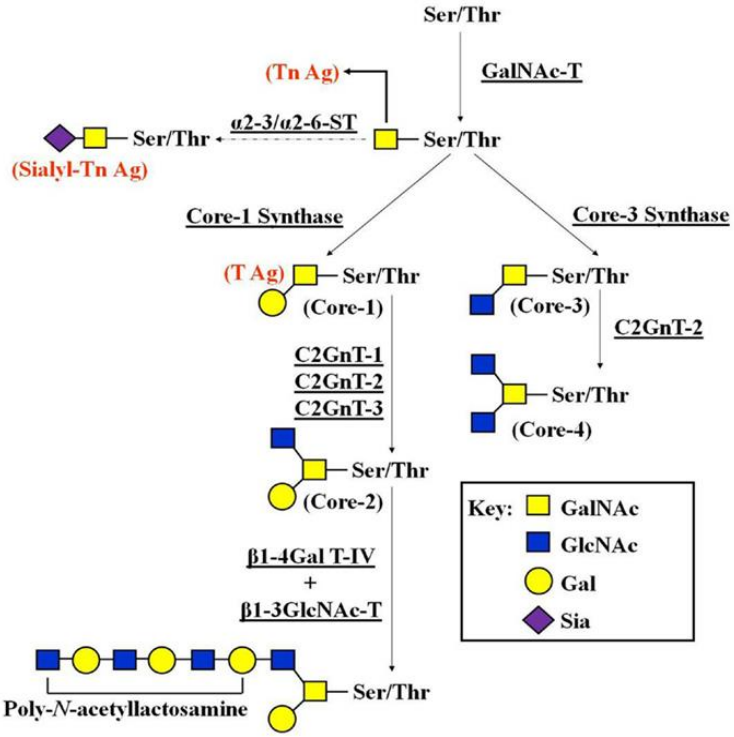


Figure 2 | Schematic representation of pathways of O-glycan biosynthesis [100]. Note that the formation of STn inhibits any further elongation of the O-glycan chains.

From a standard point of view, STn expression has been correlated with decreased cell-cell adhesion, increased extracellular matrix binding, migration, invasion and adverse outcome among cancer [95, 101]. However, owing to the different observed features, it was suggested that the biological function of STn in cancer development may depend on each cancer type or subtype. For instance, numerous studies have reported an association between STn expression and metastasis [102, 103]. In addition, few studies have reported the same association in colorectal cancer [104] whereas STn may not be involved in the metastatic process in ovarian cancer [105].

In the immune context, STn is known to allow cells to escape immune surveillance as mucins bearing STn appear to inhibit natural killer (NK) cells cytotoxicity therefore impairing its function [106]. Proteins carrying this glycan structure are commonly released from the cell-surface therefore contributing to the elevation of STn concentrations in serum (CA72-4 test) in gastric, colorectal and pancreatic carcinomas.

The abnormal synthesis of STn can arise from the overexpression of the ST6GalNAc-I, its major biosynthetic enzyme or decreased core synthesis [101].

Somatic inactivation of the Cosmc gene can also lead to STn expression through the action of ST6GalNAc-I, an evidence observed in colon cancer and in melanoma cell lines [107]. As STn is increasingly considered a tumor marker in a variety of tumor types, vaccines using tumor-associated glycans coupled with immunogenic carriers are emerging as potential therapeutic strategies against cancer. Theratope, an anti-cancer vaccine, despite promising results in animal and human tests for breast, ovarian and colorectal cancers [101, 108] failed in phase III trials for metastatic breast cancer [109].

3.1.2. Sialylation

Sialylated carbohydrates have important roles in many processes such as cell recognition, cell adhesion and cell-to-cell signaling and an increase in sialylation has been correlated with poor survival in cancer patients. Indeed, the overexpression of negative charged sialylated glycans in cancer cells promotes the detachment of cells from the tumor mass disrupting cell-cell adhesion [110]. The type 1 and type 2 chains are derived from the addition of a GlcNAc to a β 1,3- or β1,4-linked galactose respectively. The substitution of the α2,3-sialylated type 1 and type 2 (also called N-acetyllactosamine, Galβ1–4GlcNAc units) chains by a fucose giving rise to sLe^a and sLe^x respectively, appear to be a cancer-associated mechanism correlated with poor prognosis [92]. The comprehension of the role of these antigens in cancer began in the 80s when several studies showed its presence in cancer specimens using monoclonal antibodies [111, 112]. Years later, another study demonstrated that sLe^a and sLe^x are selectin ligands for ELAM-1 (Endothelial Leukocyte Adhesion Molecule 1) in endothelial cells [113]. In fact, sLe^a and sLe^x are ligands for E- and P-selectins which mediate initial attachment leukocytes to the endothelium during leukocyte extravasation therefore is reasonable to postulate that cancer cells gain advantage by expressing structures that interact with endothelium components. This interaction is thought to form emboli of cancer cells and platelets that favors their arrest on endothelia, which triggers integrin-mediated signaling responsible for cell adhesion and extravasation of cancer cells determining the development of metastasis [114, 115]. In addition to its role in the metastatic cascade, sialyl Lewis antigens might also play a role in cancer progression by inducing angiogenesis, namely the sLe^x antigen [116].

Minimal structural alterations in terminal motifs derived from the competition between normal and cancer-associated structures may also be explored as novel biomarkers. An example of this resides in the competition between normal disialyl Le^a and cancer-associated sLe^a structures derived from type 1 chains in colon cancer.

Normal colon tissues mainly express the disialyl Le^a antigen while colon cancer mainly expresses sLe^a. The biosynthesis of these two antigens differ in an additional step of α-2,6 sialylation of the α-2,3 sialylated type 1 chains mediated by ST6GalNAc-VI before the final step of α-1,4 fucosylation mediated by Fuc-TIII. In colon cancer the expression of ST6GalNAc-VI is downregulated therefore resulting in the mobilization towards the synthesis of the sLe^a antigen [117]. Additionally, the competitive formation of alternative structures derived from type II chains in normal colon might also contrast with the formation of sLe^x structures in colon cancer. As such, the Sd^a [118], the sialyl 6-sulfo Le^x [119] and the 3-sulfo Le^x [120] are structures that are strongly expressed in normal colon but poorly expressed in colon cancer.

Additionally, other α2,3 sialylated structures have been observed in cancer. For instance, the impact of sialylation was observed in colorectal cancer where the presence of α2,3 sialylated structures showed a positive correlation with lymph node metastasis and lymphatic invasion [121]. Also, elevated levels of α2,3sialyltransferases were seen in breast cancer, particularly ST3Gal-III and ST3Gal-I [122].

Apart from α2,3 sialylation, the increase in sialylation is often manifested by the attachment of α2,6-linked sialic acids to either type II *N*-acetyllactosamine (Sia6LacNAc) or GalNAc residues in O-glycans (this last is discussed in sections 3.1.1 and 3.2). Particularly, Sia6LacNAc chains expressed by either O-linked or N-linked glycoproteins appear to show a significant increase in cancer [123, 124]. Many malignancies including colon or gastric cancer showed an increased expression of β-galactoside α2,6-sialyltransferase I (ST6Gal-I), its major biosynthetic enzyme [125, 126]. In agreement, colon cancer cell lines grown as mice xenographs exhibited increased Sia6LacNAc and ST6Gal-I expression levels than the same cell lines grown in culture [127]. However, studies in the colon cancer line SW948 and in glioma cells revealed a negative correlation between the expression of ST6Gal-I and invasive properties thus suggesting a probable tissue-dependence between Sia6LacNAc expression and invasive growth [128, 129].

Several lines of evidence indicate that β1 integrins are substrates of ST6Gal-I. ST6Gal-I-mediated sialylation of β1 integrin might lead to cell migration and invasion through the ability of binding to extracellular substrates and induce integrin-mediated signaling as demonstrated in cell culture studies [130, 131]. In addition, α2,6 sialylation of β1 integrins appear to play a role in cancer by inhibiting the binding of galectins such as galectin-3 [132]. Galectins are lectins that bind galactose-containing oligosaccharides and have important roles in cancer contributing to tumor cell survival, metastasis, angiogenesis and, in some cases, exert a pro-apoptotic effect [133].

Aberrant glycosylation in cancer also includes an increased expression of the α2,8-linked polymer polysialic acid [134, 135]. This modification is often present in the neural cell adhesion molecule 1 (NCAM1) and is associated with increased cell motility, aggressiveness and poor outcome in many tumors such as lung and gliomas [134].

3.1.3. Fucosylation

Overfucosylation of glycans or *de novo* expression of fucosylated glycans has also been associated with cancer. These structures are synthetized by a wide range of fucosyltransferases encoded by FUT1-11 and are subdivided in core fucosylated and terminal fucosylated glycans. Core fucosylation is based in the addition of a α1,6-linked fucose to the GlcNAc residue of N-glycans, a process catalyzed by α1,6-fucosyltransferase (Fuc-TVIII) encoded by the FUT8 gene. Enhanced core fucosylation and elevated FUT8 expression are important features observed in liver, lung and breast cancers [136-138]. In fact, increased core fucosylated glycoproteins such as alpha-fetoprotein (AFP) are commonly detected in the serum of patients with hepatocellular carcinoma (HCC) [139]. A paradigmatic example regarding the role of core fucosylation in malignancy is the positive correlation between that process and the activation of the epidermal growth factor receptor (EGFR) in lung cancer cells which have been associated with tumor cell growth [137]. In turn, terminal fucosylation involves the addition of a fucose at the terminus of the O- and N-linked structures giving rise to structures such as the Lewis group antigens. Several data have showed a reduced selectin binding and metastatic ability in cancer cell lines by the knock-down of specific fucosyltransferases involved in the synthesis of the sialyl-Lewis antigen [140, 141]. The reconstitution of sialyl Lewis expression by gene transfer revealed both increased adhesion to selectins *in vitro* and metastatic ability *in vivo* [142].

3.1.4. β1,6 branching of N-linked chains

The β1,6 branching of N-linked chains involves the binding of a GlcNAc β1,6-linked to a core mannose residue. Elevated levels of β1,6 branching appear to be associated with malignant transformation in colon and breast cancers [143]. These structures arise from the action of β1,6 N-acetylglucosaminyltransferase V (GnT-V) product of the Mgat5 gene. Downregulation of GnT-V in many cancer cell lines confirmed the involvement of β1,6 branching in tumor growth and metastasis [144, 145]. Other studies have also demonstrated a positive correlation between Mgat5

expression and tumor metastasis and progression [146, 147]. This is not a surprisingly feature since Mgat5 is regulated by the Ras pathway which is highly activated in cancer Branched N-glycans often present a polylactosaminic (N-acetyllactosamine sequences) chain followed by a Lewis type antigen termination. β1,6 branching polylactosaminic chains are ligands for galectins which are involved in many cancer-related features as stated above [148]. However, other findings showed an inverse correlation between GnT-V expression and prognosis and histology in non-small cell lung cancer [149]. Furthermore, HCC patients with no or low expression of GnT-V were more willing to recur than those with high expression [150].

In contrast, the formation of β1,4 bisecting GlcNAc N-glycans mediated by the enzyme β1,4 N-acetylglucosaminyltransferase III (GnT-III) encoded by the Mgat3 gene suppresses the formation of branched structures due to the competition between GnT-III and GnT-V [151, 152]. For instance, high metastatic B16 melanoma cells expressing Mgat3 led to the suppression of lung metastasis in mice [153]. Even though some papers describe a role for bisecting GlcNAc structures in promoting tumor growth, the bulk of data describes the opposite. GnT-III appears to counteract GnT-V function and so lead to tumor suppression by at least two mechanisms: through E-cadherin regulation which induces the stabilization of the adherent junctions [154, 155] and by decreased interactions between cell surface integrins and ECM components [155-157].

3.2. Altered patterns of Protein Glycosylation in Bladder Cancer

Alternations in protein glycosylation patterns have also been relatively well documented in BC. These include loss of ABO(H) blood group determinants in secretor (Se) individuals, changes in Lewis antigen patterns and overexpression of simple mucin-type O-GalNAc antigens.

Several studies have reported the loss of ABO(H) blood group determinants in the “apparently” normal and neoplastic urothelium in bladder tumors. However, that event is significantly more pronounced in the neoplastic urothelium when compared with the histologically normal one. Other papers also correlated the loss of ABO antigens with invasive potential of the cells as well with advanced forms of the bladder cancer disease [158, 159].

The oversialylated forms of the Lewis antigens Le^a and Le^x, sLe^a and sLe^x have also been associated with malignant transformation of the bladder. The sialylated form sLe^a has been found in bladder dysplasia, carcinoma *in situ*, non-invasive and invasive

carcinomas of the bladder [160]; however no association was established between its presence and invasive or metastatic potential. Inversely, the presence of the sLe^x was reported as a predictor of invasive and metastatic potential in BC [161].

In addition, the expression of β,1-6 branching *N*-linked oligosaccharides and the GnT-V enzyme were closely related to low malignant potential and good prognosis of patients with BC [162].

Finally, increased levels of simple mucin-type O-glycans have also been observed in bladder cancer. The presence of Tn and T antigens and its correlation with recurrence and metastasis was provided by several authors [159, 163]. There is also a line of evidence regarding the role of ST3Gal-I in the sialylation of the T antigen which positively correlates with malignancy and recurrence in BC [164]. In addition to these findings *Ferreira et al*. has recently observed that approximately 75% of the high grade bladder tumors (NMIBC and MIBC) expressed STn [10]. Inversely, about 80% of low grade NMIBC and the healthy urothelium did not express the STn antigen. Moreover, STn positivity was found in quiescent or non-proliferative areas of the tumor recognized as sites with a high capacity in overcoming chemotherapy treatments. *In vitro* assays also showed the association between the expression of STn and increased cell motility and invasion capability [10]. Altogether, these evidences provide a connection between the STn expression and malignancy in bladder cancer.

Other studies also revealed the role of the STn antigen in inhibiting immune surveillance by at least two mechanisms: first, it impairs dendritic cell (DC) recognition and maturation by hindering the expression of MHC-II and co-stimulatory molecules. Second, STn endows DCs with a tolerogenic function by hindering the expression of inflammatory cytokines that polarize T cells toward the Th1 phenotype. This results in the incapacity in creating an anti-tumor response [165]. Considering these results and the association between STn and low proliferative areas of the tumor, therapies combining Theratope or other STn-based vaccine and anti-proliferative drugs might be a step forward in advanced BC therapy [10].

3.3. Protein glycosylation features in chemoresistance

In the past few years, some studies have been pointed out a relation between resistance to chemotherapeutic drugs and the alteration in the glycosylation patterns. Alterations in the expression of key glycosyltransferases appear to play an important role in the development of drug resistance. In particular, ST6Gal-I might be the driving force towards resistance to cisplatin in ovarian cells. Recently, it was found that cisplatin-resistant ovarian cells exhibited elevated ST6Gal-I levels thus suggesting the involvement of receptor α2,6-sialyalation in tumor cell survival [166]. In fact, ST6Gal-I appears to be involved in the blockage of apoptosis-related pathways. As such, increased sialylation of the death receptor Fas was demonstrated to inhibit receptor-internalization and apoptosis [167]. Other studies also revealed the involvement of ST6Gal-1 in blocking apoptosis through the sialylation of Tumor Necrosis Factor Receptor 1 (TNFR1) [168] and also galectin-3 substrates, a well-known inducer of apoptosis [133, 169]. Moreover, the expression of ST6Gal-I correlated with the expression of the stem cell markers ALDH1 and CD133 indicating a connection between ST6Gal-I and chemoresistance [170]. Additionally, alteration in the expression of N-glycan glycosyltransferases involved in the elongation of the N-linked chains such as GnT-V might also be associated with drug resistance among different types of carcinomas [171-173].

Resistance to conventional chemotherapeutic agents might also be associated with N-glycosylation alterations of ABC transporters involved in drug efflux. The MRP1 transporter is one of those transporters and was found less glycosylated in cisplatin-resistant epidermoid carcinoma cells. This was accompanied by reduced cell-surface expression and intracellular mislocalization [174]. These observations were reinforced in oxaliplatin-resistant ovarian cell lines where reduced N-glycosylation of MRP1 and MRP4 were correlated with enhanced expression of these transporters and therefore promoted resistance to oxaliplatin [175]. In addition, glycosylation alterations of other ABC transporters were also noticed and correlated with their altered cellular localization [176]. In spite of the association between defects in glycosylation of ABC transporters and drug resistance, controversial data have also been reported which means that more investigation related to this subject is needed.

4. Aims and scopes

Preliminary studies from our group suggest that profound de-regulations of protein O-glycosylation pathways translated by STn overexpression associate with late stage bladder cancer, invasive phenotypes and possibly chemoresistance. This work now aims to gain more insights on the biomarker potential of STn in the context of advanced stage disease and response to chemotherapy and identify putative targets for designing highly specific targeted therapeutics.

Specific objectives are the following:

I. Define the role of the STn antigen in the prognostication of MIBC disease;

II. Include STn expression in a recently proposed molecular model for bladder cancer prognostication based on the degree of tumor differentiation, towards precision medicine settings;

III. Define the role of the STn antigen as a chemoresistance biomarker;

IV. Mine the O-Glycoproteome of STn-expressing proteins on chemoresistant cells envisaging putative targets to improve bladder cancer management.

These objectives were comprehensively addressed in Chapters II-IV of this thesis. Accordingly, chapter II focused on responding to objective I; chapter III responded to objectives II and III and finally chapter IV responded to objective IV. The chapters followed a research paper format, including an abstract, a brief introduction, material and methods, results and discussion. Finally, chapter V provided an integrative overview of the results, concluding remarks and future prespectives.

Chapter II | Sialyl-Tn overexpression is associated with advanced bladder tumors

(Part of the data presented in this chapter has been included in a publication in Plos One – see Appendix A)

Abstract

Muscle invasive bladder cancer (MIBC) constitutes the second most cause of death among genitourinary cancers. Treatment consists of radical cystectomy and cisplatin-based chemotherapy regimens that fail avoiding relapse and disease dissemination. Additionally, molecular heterogeneity within invasive tumors has been related with variations in clinical outcome observed even in patients with similar histopathological nature. Thus, these concerns have delayed the introduction of biomarkers capable of aiding treatment procedures. Altered glycosylation patterns translated by the expression of the sialyl-Tn antigen and its precursor Tn may hold potential for patient stratification and guided therapy. Therefore, a retrospective study including 127 bladder tumors (47 NMIBC and 80 MIBC) was screened for STn and Tn antigens. In our series, Tn antigen was not linked with stage or outcome. Inversely, STn was more associated with MIBC than with NMIBC ($p<0.001$) and decreased cancer-specific survival among both NMIBC (log rank $p = 0.020$) and MIBC (log rank $p= 0.043$). Moreover, STn was found in the invasive front of MIBC tumors and in the metastasis of all STn^+ tumors denoting a role in the metastasis formation. In conclusion, STn appears to be a biomarker of poor prognosis and may constitute a valuable target for guided therapy on advanced bladder tumors.

Keywords: protein glycosylation, bladder cancer, sialyl-Tn, personalized biomarkers

Introduction

Bladder cancer constitutes the most common type of cancer of the urinary tract and the second most cause of death among genitourinary cancers. This disease is divided in non-muscle invasive bladder cancer (NMIBC) and muscle-invasive bladder cancer (MIBC) with significant poor prognosis [177]. Approximately 80% of the patients present MIBC lesions at diagnosis which present high rate of recurrence (~75%) and low rate of progression (~10%) to muscle-invasive disease. In turn, 20% of all diagnosed cases are MIBC, the majority of which diagnosed in patients without a prior history of disease. Treatment of MIBC consists of radical cystectomy and neo(adjuvant) cisplatin-based chemotherapy regimens [5]. Due to the significant molecular

heterogeneity presented by invasive tumors which sometimes is reflected on tumors with similar histopathological features, it is impossible based on histology alone to predict clinical prognosis. Moreover, 50% of MIBC cases develop metastasis within five years, a fact that supports the urgency in the identification of biomarker panels capable of prognostication and the development of specific targeted-therapeutics [3]. Recent studies in a small retrospective series of bladder tumors addressed the expression of the sialyl-Tn antigen (STn). STn derives from the premature stop in the protein O-glycosylation of cell-surface receptors and it was found an association between its presence and advanced stage of the disease [10]. Moreover, STn expression was absent from most low-grade NMIBC as well as from the normal urothelium [10]. Several *in vitro* studies also showed a correlation between STn expression and malignancy processes such as impaired integrin function, enhanced cell motility, invasion and epithelial-to- mesenchymal transition [95, 178]. Furthermore, this antigen was associated with protection from host immune responses by impairing dendritic cell maturation and anti-tumor T-cell responses [165]. All of these observations suggest that STn may play a role in disease outcome. Concerning the STn precursor Tn, several studies suggest its involvement in oncogenic events [92], however none has explored its expression in bladder tumors. For all these reasons, this chapter is devoted to define a role for STn and also its precursor Tn in the prognostication of MIBC disease.

Materials and Methods

Population

This work was performed in a retrospective series of 127 formalin-fixed paraffin-embedded bladder tumors. The male/female gender ratio was of 104:23 and the median age was 72 years [42-86]. Forty seven of the examined tumors were considered as NMIBC (27 Ta and 20 T1 tumors) and eighty as MIBC (22 T2, 36 T3 and 21 T4 tumors). Sixteen were low-grade and 111 were high-grade tumors, according to the 2004 WHO grading criteria. Metastasis was present in 53% of the invasive tumors. Cancer-specific survival (CSS) was defined as the period between the tumor removal by surgery and either patient death by cancer or the last follow-up information.. All tumor samples were revised by a pathologist, regarding 2004 WHO grading criteria. All procedures were performed after patient's informed consent and approved by the

Ethics Committee of IPO-Porto. All clinicopathological information was obtained from patients' clinical records.

Immunohistochemistry

Formalin-fixed, paraffin-embedded tissue sections were screened for STn and its precursor Tn by immunohistochemistry using the strepavidin/biotin peroxidase method. Briefly, 3 μm sections were deparaffinised with xylene, rehydrated with graded ethanol series, microwaved for 15 min in boiling citrate buffer (10mM Citric Acid, 0.05% Tween 20, pH 6.0), and exposed to 3% hydrogen peroxide for 20 min. STn expression was performed using anti-STn mouse monoclonal antibody (clone TKH2, non-commercial hybridoma) at a dilution of 1:20 in PBS, after overnight (o.n.) incubation at 37°C. In turn, Tn expression was performed using anti-Tn mouse monoclonal antibody (clone IE3, non-commercial hybridoma) at a dilution of 1:5 in PBS after o.n incubation at 37°C. After blockage with BSA (5% in PBS), the antigens were identified with UltraVision HRP Detection System Kit (Thermo Scientific) followed by incubation with 3,3-diaminobenzidine tetrahydrochloride (Impact Dab, Vector Labs) for color development. Finally, the slides were counterstained with hematoxylin for 1 min. The negative control sections were performed by adding BSA (5% in PBS) devoid of primary antibody. Positive controls were known positive bladder and gastric tumors for the antigens under study. A semi-quantitative approach was established to score the immunohistochemical labeling based on the extent and intensity of staining. The STn expression was assessed double-blindly by two independent observers and validated by an experienced pathologist. Whenever there was a disagreement, the slides were reviewed, and consensus was reached.

Statistical analysis

Statistical data analysis was performed with IBM Statistical Package for Social Sciences—SPSS for Windows (version 20.0). Chi-square analysis was performed to compare categorical variables. Kaplan-Meier survival curves were used to evaluate correlation between STn expression and CSS and were compared using log-rank test.

Results

Tn and STn antigen expression in bladder cancer

Altered patterns of protein glycosylation translated by the expression of Tn and its sialylated counterpart STn were evaluated by immunohistochemistry envisaging biomarkers of poor cancer-specific survival.

As represented on table I, our series was composed of 47 NMIBC and 80 MIBC. The Tn expression was observed in approximately 10% of all NMIBC and MIBC (p=0.461). In turn, STn expression was observed in approximately 40% of NMIBC tumors and in 70% of MIBC tumors (p=0.002). Therefore, special attention was set on the identification of biomarkers for advanced bladder tumors.

Table I - Association between the evaluated markers and the stage of disease. Tn analysis only included 49 cases of the 80 MIBC.

		Bladder Cancer		
		NMIBC n(%)	MIBC n(%)	*p*
Tn				
	Negative	41 (87,2)	45 (91,8)	
	Positive	6 (12,8)	4 (8,2)	0,461
STn				
	Negative	27 (57,4)	24 (30.0)	
	Positive	20 (42,6)	56 (70.0)	0,002

Tn expression did not exceed 5% of the tumor area. In turn, STn expression was focal and did not exceed the 30% of the tumor area for positive cases irrespectively of their histological origin. In spite of the observation of cytoplasmic staining STn was predominately expressed at the cell membrane. STn was mainly expressed by dedifferentiated cells in T1 tumors (60%) and in tumors invading *muscularis propria* (60-75%) while positive Ta was lower than 30% (p<0.001) (Fig.3A). Considering only Ta tumors, STn expression was mainly found in superficial layers away from the fibrovascular support while STn positive cells in T1 tumors were found accompanying and/or invading the basal layer (Fig.3B). Concerning MIBC cases, STn

positive cells were mostly observed in the invasion fronts of the tumor and/or inside the vessels (Fig.3B).

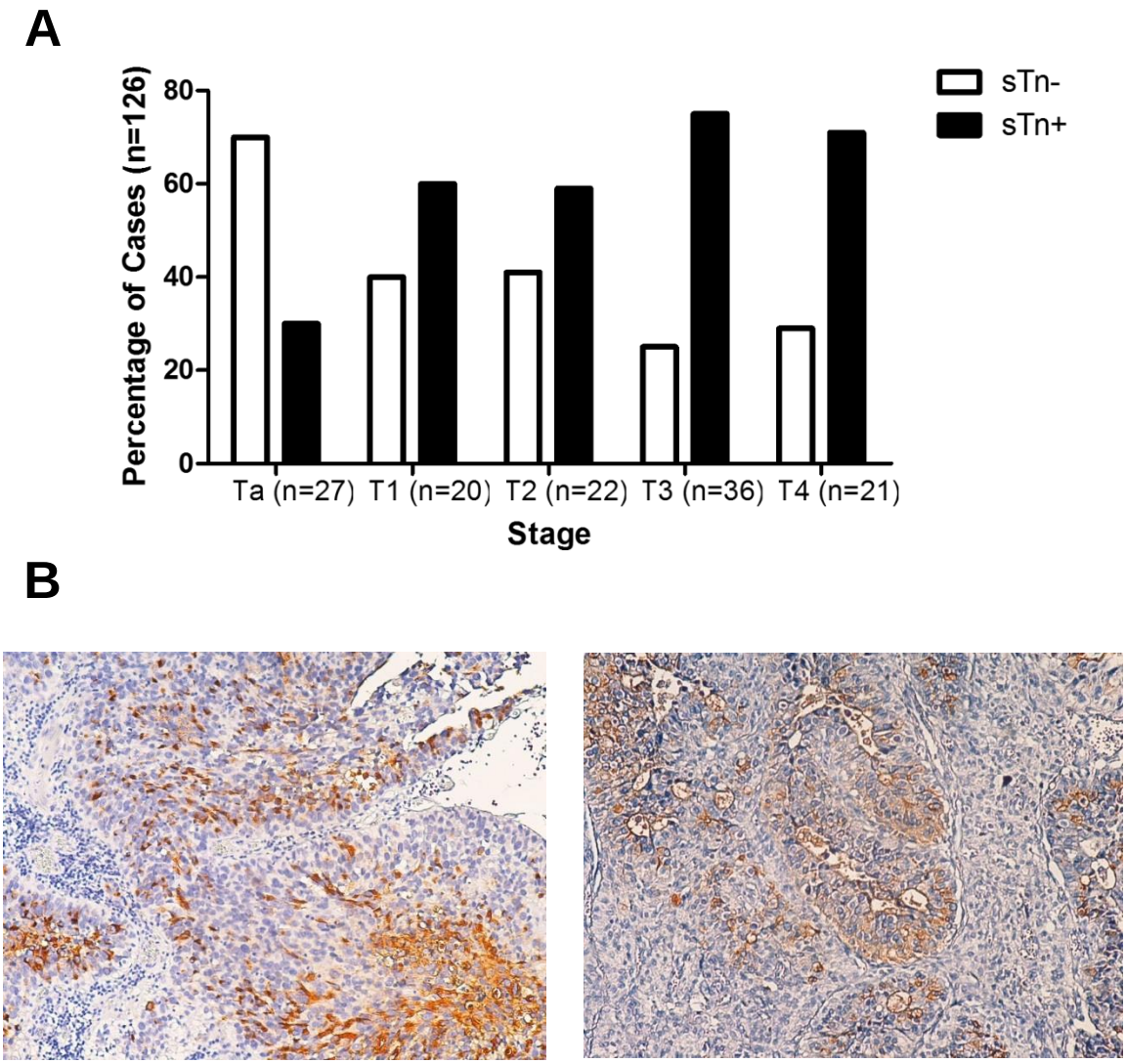


Figure 3 | STn expression in different bladder tumors stages. (A) Distribution of tumors among NMIBC (Ta and T1) and MIBC (T2, T3 and T4). **(B)** Representative areas of NMIBC tumors showing STn positive cells away from fibrovascular support (left panel) and MIBC tumors showing STn positive cells in the tumor invasion front and inside the vessels suggesting its possible involvement in the metastasis (right panel).

In addition, STn was associated with lymph-node metastasis (p=0.016; table II) and its expression was found in the metastasis of all STn positive tumors. These observations suggest a role for STn in tumor invasion and disease dissemination.

Table II - Association between STn and the stage of disease, lymph-node metastasis, recurrence and metastasis formation in MIBC patients.

		STn$^-$ n (%)	**STn$^+$ n (%)**	***p***
Stage	T2	9 (37.5)	13 (22.6)	0.206
	T3/T4	15 (62.5)	42 (76.4)	
Lymph-node metastasis	N_0	10 (90.9)	17 (48.6)	0.016
	N_1	1 (9.1)	18 (51.4)	
Recurrence	No	11 (61.1)	16 (41.0)	0.248
	Yes	7 (38.9)	20 (59.0)	
Metastasis formation	No	15 (62.5)	23 (41.1)	0.079
	Yes	9 (37.5)	33 (58.9)	

Tn, STn and Cancer-Specific Survival

Next, a Kaplan-Meyer analysis was used in order to evaluate if STn and Tn could discriminate groups presenting different CSS. We found that tumors bearing STn presented lower CSS among NMIBC (p=0.020; Fig.4A) and MIBC (p=0.043; Fig.4B), Moreover, considering NMIBC, STn expressing T1 tumors presented lower CSS than negative tumors (p <0.05). In turn, Tn positive tumors showed no differences in CSS when compared to Tn negative lesions, irrespectively of their stage.

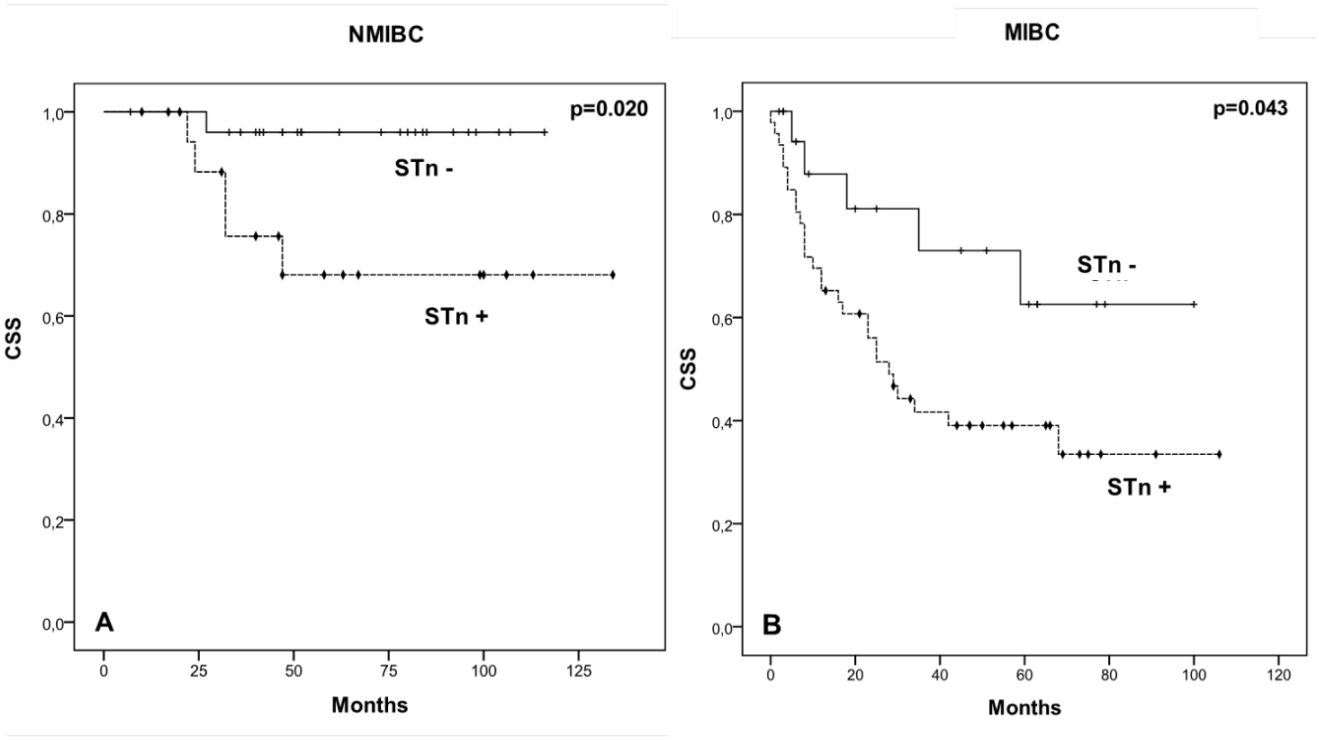


Figure 4 | Effect of STn expression in cancer-specific survival (CSS). Kaplan–Meier analysis showing the association between STn and CSS in: **(A)** NMIBC patients; **(B)** MIBC patients. Comparison performed by log-rank test (A: p=0.024; B: p=0.043); + censored STn negative tumors; ♦ censored STn positive tumors.

Discussion

Molecular heterogeneity within advanced bladder tumors is a major concern leading to variable clinical outcomes to conventional therapeutics (cystectomy and cisplatin-based chemotherapy regimens. Moreover, treatment has not advanced for several decades therefore new therapies for disease personalization are needed.

In a previous explorative study, it was observed an association between the overexpression of the truncated O-glycan structure STn and advanced bladder tumors [10]. In this study, we started to evaluate the expression of its precursor Tn which may be implicated in oncogenic events however nothing is known with regards to its expression in bladder tumors. We found that this antigen presented a low expression in bladder tumors and was not associated with any stage of the disease. This observation suggest that Tn is rapidly sialylated or extended with more complex glycans in bladder tumors. It was also confirmed that STn is more associated with muscle invasive than with non-muscle invasive disease, a fact that reinforces the role of sialylation in advanced bladder tumors. Furthermore, STn was found in the invasion front of

advanced tumors and in the metastasis of all STn positive patients. These observations suggest that STn is associated with metastasis formation and disease dissemination. Additionally, a correlation between STn positive tumors and lower CSS in both NMIBC and MIBC was also provided, a notion that supports previous observations for digestive track tumors [179, 180]. In accordance with these findings, STn was found to be involved in the modulation of cancer cells in a way that favors malignancy in gastric [95], breast [178] and bladder [10] cancers. As such, STn was found to impair cell-cell adhesion and integrin function, enhance invasion and cell motility [95] as well as epithelial-to-mesenchymal tramsition, an event that leads to metastasis and disease dissemination in cancer cells [181]. We have also showed that STn is involved in immune escape not only by impairing dendritic cells maturation but also by hindering the expression of inflammatory cytokines that polarize T cells toward the Th1 phenotype and trigger T-cell responses [165]. All of these statements reinforce the role of the STn antigen in malignancy and disease dissemination, however guided-therapy towards these malignant phenotypes is still missing.

In resume, we have revealed that STn is associated with poor prognosis particularly in MIBC disease. Thus, the identification of STn-expressing proteins may provide new insights about the role of these glycans in bladder cancers as well as novel therapeutic targets that may ultimately improve bladder cancer management.

Chapter III | Molecular profiling of advanced stage bladder tumors: adding Sialyl-Tn towards precision medicine

Abstract

A recent molecular classification has been proposed to improve the stratification and prognostication of bladder tumors, which has been based on histological features alone. Accordingly, a Keratin profile has allowed, to some extent, distinguishing well differentiated luminal tumors ($KRT14^{-}KRT5^{-}KRT20^{+}$) with better prognosis from dedifferentiated basal-like lesions (KRT14 and/or KRT5 KRT20-), with reduced survival and higher resistance to conventional chemotherapy. This work now aimed to improve the predictive capability of this model based on the inclusion of STn overexpression. Therefore, in a retrospective series of 129 MIBC tumors we used Keratin expression profiling in a set of cystectomy (n=80), adjuvant (n=20) and neoadjuvant-treated (n=29) patients. It was found that basal-like tumors had worse cancer-specific and disease-free survival than luminal tumors. Moreover, it was also found that STn positive luminal and basal-like tumors had worse CSS than STn negative luminal and basal-like tumors, respectively. Furthermore, STn was present in the metastasis of 70% of patients that had disease progression after adjuvant chemotherapy, suggesting its association with chemoresistance phenotypes. Also supporting these observations, STn positive patients that underwent neo-adjuvant chemotherapy maintained their STn positivity after treatment and a marked basal phenotype, irrespectively of the initial stage of differentiation of the tumor. To confirm these results, two UC cell lines (T24 and HT1376) were submitted to cisplatin and it was found that STn expression maintained unchanged after two cycles of treatment with cisplatin. An enrichment in basal-like cells amongst chemoresistant clones was also evident. Concomitantly, chemoresistant cell transcripts analysis revealed the activated EMT programs, associated with the enhanced migrating and disseminating capabilities, and the evasion of apoptosis in response to DNA damage. Altogether, these findings reinforce the notion that STn is a biomarker of aggressiveness and chemoresistance and the importance of developing targeted therapeutics based on this antigen. Moreover work also supports the inclusion of STn in bladder cancer predictive molecular profiles towards patient tailored precision medicine settings.

Keywords: protein glycosylation, bladder cancer, sialyl-Tn, personalized biomarkers; chemoresistance; keratins

Introduction

Molecular heterogeneity is a major concern in MIBC management, leading to the observation of distinct clinical outcomes to conventional treatments (radical cystectomy and (neo) adjuvant chemotherapy) in tumors showing similar histopathological nature. The introduction of personalized or individualized medicine (precision medicine) offers potential to improve disease outcome based on the refinement of prognosis and predicting response to treatment. Therefore, specific biomarkers capable of patients' stratification and early identification of groups facing worst prognosis as well as predicting response to therapy are warranted.

A recent molecular model has been proposed to improve the stratification of bladder tumors, based on alterations in the degree of differentiation of the tumors translated by keratins (KRTs). KRTs are the largest group of Intermediate Filament proteins typically expressed in epithelial cells and comprise the majority of IF genes in the human genome. KRTs are differentially expressed during epithelial tissue differentiation, a phenotype that is often conserved in neoplastic transformation. Namely, there is a clear hierarchy in the bladder epithelium, translated by basal, intermediate and differentiated cells, with distinct KRT profiles. KRTs such as KRT5 and KRT20 may be used to clearly differentiate cells composing the urothelium [69]. Based on these observations, Damrauer *et al.* demonstrated that MIBC could be divided in "basal-like" and "luminal" subtypes and these showed similarities to intrinsic breast cancer subtypes [182]. It was also proved that KRTs are associated with BC differentiation and that luminal MIBC are enriched for KRT20 and basal-like MIBC are enriched for KRT14 and/or KRT5 [182]. Moreover this study revealed that the basal-like subtype in the Danrauer´s classification is significantly associated with poor overall survival showing the prognostic utility of stratification of patients by BC subtypes. In addition, basal-like tumors have proven enriched for cancer stem cells phenotypes and significant resistance to conventional chemotherapy drugs (cisplatin and gemcitabine) [182]. However, the introduction of novel molecules in this model is necessary to improve their predictive capability.

In a previous explorative study, our group identified a link between STn and advanced bladder tumors by showing its overexpression among approximately 70% of high-grade bladder tumors. Moreover, STn was found to impair integrin function, enhance cell motility, invasion and EMT and protect BC cells from host immune responses. As demonstrated in the previous chapter, STn expression is more

associated with MIBC than NMIBC in a larger set of patients as well as its association with decrease survival. Altogether these facts reinforce the notion that the STn antigen is a biomarker of poor prognosis particularly in MIBC disease

Based on these observations we hypothesize that the introduction of STn on molecular model for predicting tumor differentiation based on KRTs profiling may help managing bladder cancer patients.

Materials and Methods

Population

This study was conducted in a retrospective series of 129 cases with muscle-invasive bladder cancer. Patients underwent consultation, surgery and treatment in the Portuguese Institute of Porto, between 2005 and 2013. The male/female gender ratio was of 113:16 and the median age was 69 years [28-84]. Tumor staging was obtained from patients´ clinical records and further reviewed by a pathologist MD according to the current TNM system. Of the primary tumors, 32 cases were considered stage T2, 56 stage T3 and 35 stage T4 (for further analysis T3 and T4 staged tumors were evaluated together and compared against T2 staged tumors). Correspondent metastasis was found in 40 cases of all primary tumors. Cystectomy was the main treatment (n=80) followed (adjuvant, n=29)) or preceded (neoadjuvant, n=20)) by chemotherapy. Tumor recurrence was defined as the appearance of a tumor once treatment has begun. Both recurrence and metastasis formation were considered as loco-regional if affected the lymph nodes or systemic (distant metastasis). Cancer-specific survival (CSS) was defined as the period between the tumor removal surgery and patient death from cancer and the last follow-up information. Disease-free survival (DFS) was defined as the period between the tumor removal by surgery and the detection of a metastasis or the last follow-up information. All procedures were performed after patient's informed consent and approved by the Ethics Committee of IPO-Porto. All clinicopathological information was obtained from patients' clinical records. All tumor samples were revised by a pathologist, regarding 2004 WHO grading criteria. Table III summarizes all the clinical information reported above.

Table III – Clinicopathological information and treatment of the studied samples
ND – Not Determined

		All cases n (%)	Cystectomy n (%)	Neoadjuvant chemotherapy n (%)	Adjuvant chemotherapy n (%)
Stage	T2	32 (26,0)	22 (27,8)	5 (33,3)	5 (17,2)
	T3	56 (45,5)	36 (45,6)	7 (46,7)	13 (44,8)
	T4	35 (28,5)	21 (26,6)	3 (20,0)	11 (38,0)
Lymph-node metastasis	N_0	42 (33,1)	27 (34,2)	11 (57,9)	4 (13,8)
	N_1	47 (37,0)	19 (24,0)	6 (31,6)	22 (75,9)
	N_x	38 (29,9)	33 (41,8)	2 (10,5)	3 (10,3)
Recurrence	No	46 (45,5)	28 (49,1)	6 (35,3)	12 44,4)
	Yes	55 (54,5)	29 (50,9)	11 (64,7)	15 (55,6)
	ND	28	23	3	2
Type of recurrence	Loco-regional	18 (34,6)	7 (25,9)	4 (40,0)	7 46,7)
	Systemic	34 (65,4)	20 (74,1)	6 (60,0)	8 (53,3)
Metastasis formation	No	46 (35,7)	38 (47,5)	7 (35,0)	1 (3,4)
	Yes	83 (64,3)	42 (52,5)	13 (65,0)	28 (96,6)
Type of metastasis	Loco-regional	41 (49,4)	17 (40,5)	4 (30,8)	20 (71,4)
	Systemic	42 (50,6)	25 (59,5)	9 (69,2)	8 (28,6)

Immunohistochemistry

Formalin-fixed, paraffin-embedded tissue sections were screened for STn and for Keratins 5, 14 and 20 by immunohistochemistry using the strepavidin/biotin peroxidase method. Briefly, 3 μm sections were deparaffinised with xylene, rehydrated with graded ethanol series, microwaved for 15 min in boiling citrate buffer (10mM Citric Acid, 0.05% Tween 20, pH 6.0), and exposed to 3% hydrogen peroxide for 20 min. STn expression was performed using anti-STn mouse monoclonal antibody (clone TKH2, non-commercial hybridoma) at a dilution of 1:5 in PBS, after overnight (o.n.) incubation

at 37°C. Keratin 5 expression was performed with KRT5 antibody (Monoclonal Rabbit Anti-Human Anti-Cytokeratin 5 antibody; Clone EP1601Y; Abcam) at a dilution of 1:100 in PBS, after 1h incubation at 37°C. Keratin 14 expression was accessed with the KRT14 antibody (Monoclonal Rabbit Anti-Human Anti-Cytokeratin 14 antibody; Clone EP1612Y; Abcam) at a dilution of 1:50 in PBS, after overnight incubation at 4°C. Keratin 20 expression was evaluated using KRT20 antibody (Monoclonal Rabbit Anti-Human Anti-Cytokeratin 20 antibody; Clone EPR1622Y; Abcam) at a dilution of 1:100 in PBS, after 1h incubation at 37°C.After blockage with BSA (5% in PBS), the antigens were identified with UltraVision HRP Detection System Kit (Thermo Scientific) followed by incubation with 3,3-diaminobenzidine tetrahydrochloride (Impact Dab, Vector Labs) for color development. Finally, the slides were counterstained with hematoxylin for 1 min. The negative control sections were performed by adding BSA (5% in PBS) devoid of primary antibody.

Cell Lines and Culture conditions

The T24 (grade III) and HT1376 (grade III) bladder cancer cell lines used in this work were acquired from DSMZ (Düsseldorf, Germany) and recently characterized from the genetic standpoint by our group [183]. Accordingly, the T24 cell line is representative of the FGFR3/CCND1 disease progression pathway, presenting a mutated *HRAS* and over-expression of *CCND1*. The HT1376 cell line represents the E2F3/RB1 pathway with loss of one *RB1* copy and mutation of the remaining copy. Additionally, HT1376 exhibits *PTEN* gene deletion, no alterations in *PIK3CA* and inactivation of *p53*.

The cells were cultured in RPMI 1640 (1X) + GlutaMAXTM-I medium (Gibco, Life Technologies), supplemented with 10% heat-inactivated FBS (Gibco, Life Technologies) and 1% penicillin-streptomycin (10,000 Units/mL P; 10,000 µg/mL S; Gibco, Life Technologies). Cell lines were cultured as a monolayer at 37ºC in a 5% CO_2 humidified atmosphere (normoxia), and were routinely subcultured after trypsinization before reaching 90% confluence. For drug resistance experiments, two experimental groups were considered. One group (experimental group) was exposed to two consecutive cycles of Cisplatin in a IC50 concentration (2,5 mg/mL for T24 and 4 mg/mL for HT1376 as determined by Pinto-Leite et al [183] for a 72 hour period. Cisplatin exposed cells were allowed to recover for a 30 day period and subsequently trypsinized and frozen at -80^{o}C while awaiting further analysis. A control group treated with the drug delivery was maintained under the same conditions. Cell viability was

determined using the Trypan Blue Exclusion Test of Cell Viability. Briefly, cells uptaking trypan blue were considered non-viable. Cell viability was calculated as the number of viable cells divided by the total number of cells within the grids on the hemocytometer. Two independent experiments were performed in triplicate for each cell line and condition.

Protein extraction and Slot Blot

Proteins were extracted from frozen T24 and HT1376 bladder cancer cells samples on RIPA lysis buffer (150mM NaCl, 1% NP40, 0.5% sodium deoxycholate, 0.1% SDS, 50mM Tris pH 8.0 with 10µg/mL protein inhibitor cocktail, all from Sigma) and the amount of protein in each extract was estimated with RC protein assay kit (BioRad). Five micrograms of protein were slot-blotted onto 0.45 µm nitrocellulose membranes (GE Healthcare). Protein loads were controlled using Ponceau Red (Sigma). Membranes were then blocked with 1% carbohydrate depleted carbo-free solution (Vector laboratories) for 1 h at room temperature, incubated overnight at 4ºC with anti-sTn TKH2 monoclonal antibody in culture supernatant, washed with TBS-T for 30 min, and finally incubated for 45 min with goat anti-mouse IgG1 heavy chain horseradish peroxidase conjugate (Abcam; 1:90,000 in TBS). After washing, the bound antibodies were revealed by chemiluminescence using the ECL prime Kit (BIORAD). Control samples resulted from treating cell lysates with 10U/mL α-neuraminidase from *Clostridium perfringens* (Sigma) for 90 min at 37ºC. Treatment with neuraminidase removes the sialic acid from STn originating the Tn antigen (GalNAc-Ser/Thr), which is not recognized by the anti-STn TKH2 monoclonal antibody.

RNA isolation and cDNA conversion

Total RNA was extracted from Formalin-fixed, paraffin embedded tissue sections (FFPE) for KRT expression analysis and from cell lines for the genes indicated in Table IV. RNA extraction from FFPE sections was performed using “AbsolutelyRNA FFPE kit” (Stratagene, La Jolla, CA) while total RNA from cultured cells was isolated using TriPure isolation Reagent (Roche Diagnostics GmbH, Mannheim, Germany). The purity and quantity of RNA extracts was determined based on the A260/A280 ratio using Nanodrop ND1000 (Nano Drop Technologies Inc. Wilmington, DE, USA). Only ratios between 1.9 and 2.1 were considered further. Up to 2mg of total RNA from tissue

sections and total RNA from the cultured cells was reverse transcribed with random primers, using the “High Capacity cDNA Reverse Transcription Kit” (Applied Biosystems, Foster City, CA). The amplification conditions were the following: 25ºC for 10 min, 37ºC for 120 min and RT inactivation at 85ºC for 5 min. Two no-template negative controls were used. The products were amplified in a Mycycler Thermal cycler (Bio-Rad).

mRNA expression analysis

The expression levels of the whole genes, including three reference genes were assessed by TaqMan assay (Applied Biosystems), and the Assay ID provided by the manufacturer are indicated in Table IV. Real-time PCR amplification of cDNA samples was performed in a StepOne Real-Time PCR System (Applied Biosystems) using TaqMan Gene Expression Master Mix, primers and probes provided by Applied Biosystems. Thermal cycling conditions were 10 min at 95ºC followed by 45 cycles of 15 seconds (sec) at 95ºC and 1 min at 60ºC. All the reactions were run in duplicate. During the cDNA exponential amplification the product formation was proportional to the fluorescence emission resulting from the TaqMan probe degradation. The relative mRNA levels were calculated by adapting the $2^{-\Delta\Delta Ct}$ formula. *HPRT, B2M and ActB* genes were selected for normalization from a set of 4 housekeeping genes, *ACTB*, *GAPDH*, *HPRT* and *18S*, since they present higher stability among the bladder tumor samples. Gene expression data was interpreted using the CluePedia+ClueGo for Cytoscape [184, 185].

Table IV - TaqMan Gene Expression Assay references used to assess transcript levels for the 27 determined genes.

Cell Function	Gene	TaqMan Gene Expression Assay Reference
Self-renewal and stemness	*NANOG*	Hs04260366_g1
	LIN28A	Hs01552405_g1
	OCT-4	Hs04260367_g1
	KLF9	Hs00230918_m1
	KLF4	Hs00358837_g1
	SOX2	Hs01053049_s1

Epithelial phenotype	*CDH1*	Hs01023894_m1
	DSP	Hs00950591_m1
	EpCAM	Hs00901885_m1
Mesenchymal phenotype	*FN1*	Hs00365052_m1
	CDH2	Hs00983056_m1
	VIM	Hs00185584_m1
ECM synthesis and promotion of changes to cell shape	*SPARC*	Hs00234160_m1
EMT	*SNAI1*	Hs00195591_m1
	SNAI2	Hs00950344_m1
	TWIST1	Hs01675818_s1
	TWIST2	Hs00382379_m1
	ZEB1	Hs01566410_m1
	ZEB2	Hs00207691_m1
	RUNX1	Hs01021971_m1
	RUNX2	Hs01047973_m1
Cell protection	*KRT5*	Hs00934200_g1
	KRT14	Hs00559328_m1
	KRT20	Hs00300643_m1
Reference genes	*B2M*	Hs00984230_m1
	HPRT	Hs99999909_m1
	ActB	Hs99999903_m1

Data analysis

Statistical data analysis was carried out using the computer software IBM Statistical Package for Social Sciences—SPSS for Windows (version 20.0). Chi-square analysis was used to compare categorical variables. Kaplan-Meier survival curves were used to evaluate correlation between the different subtypes and CCS/DFS and were compared by log-rank statistical test.

Results

Stratification of MIBC tumors based on keratins expression patterns

Tumors were first categorized based on the keratin profiles used on Damrauer stratification, which translates different states of urothelium differentiation. Accordingly, $KRT14^{+}KRT5^{+}KRT20^{-}$, $KRT14^{+}KRT5^{-}KRT20^{-}$ and $KRT14^{-}KRT5^{+}KRT20^{-}$ expression profiles were considered as basal-like subtype and $KRT14^{-}KRT5^{-}KRT20^{+}$ was considered as luminal subtype. Figure 5 represents the distribution of the tumors according to the two subtypes and shows a predominance of basal-like tumors in relation to luminal lesions.

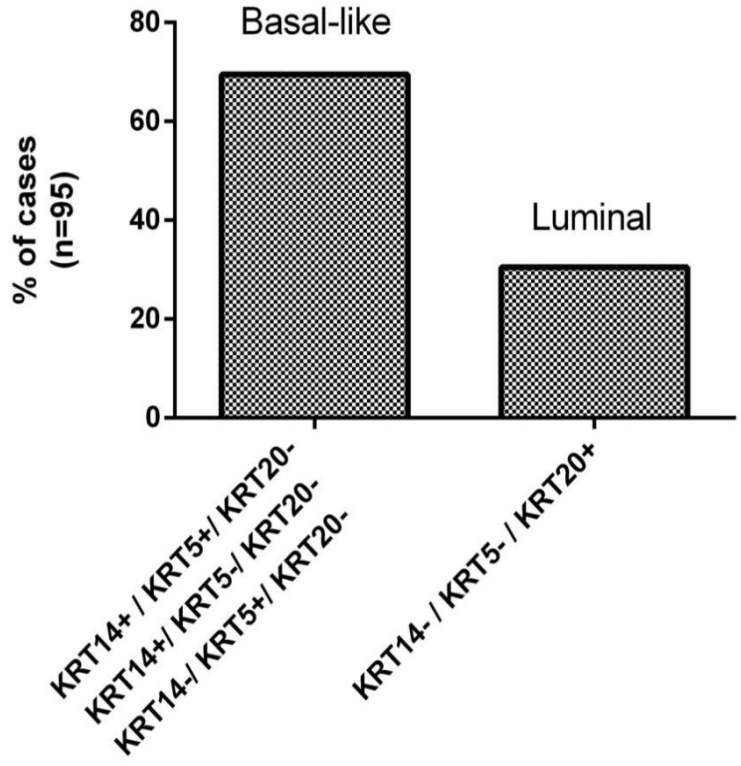


Figure 5 | Schematic representation of the keratin expression profiling of our studied sample (n=95). Stratification of the studied sample using Damrauer classification of Basal-like and luminal tumors. Basal-like tumors were considered as expressing KRT14 and/or KRT5 and not KRT20 while luminal tumors were considered as expressing only KRT20.

In order to validate the results found with the assessment of mRNA expression levels by real time PCR, we evaluated the protein expression of the studied keratins in

bladder tumor tissues using an immunohistochemistry approach. Figure 6 shows the keratins expression on representative areas of tumors classified previously as basal-like and luminal. Regarding the basal-like subtype, an elevated expression of KRT14 and/or KRT 5 was observed, whereas KRT20 was not expressed in tumors of this subtype. Moreover, KRT20 expression was found only in luminal tumors, without the expression of KRT14 and KRT5. These results were in accordance with the mRNA gene expression levels.

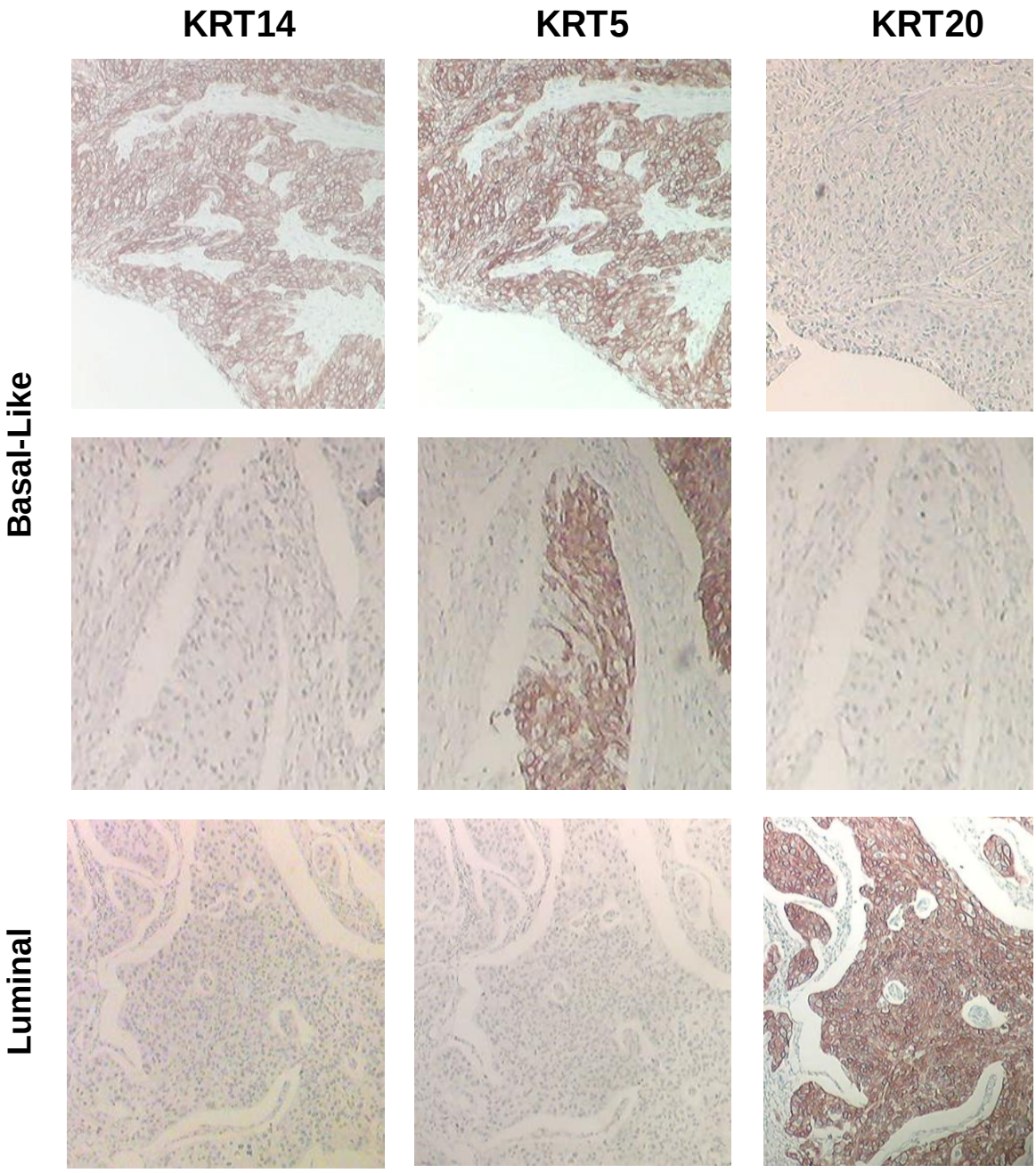


Figure 6 | Immunohistochemical staining showing the different expressions of keratins in bladder tumors (x100). Columns represent the staining of the antigen for each keratin (KRT5, KRT14 and KRT20 and the lines depicts the different subtypes studied.

KRT expression patterns in the context of BC treatment

The distribution of above subtypes according to clinicopathological variables is represented in Table V. Our results demonstrate that basal-like tumors were more pronounced in advanced bladder tumors (T3 and T4) (p=0.014). Furthermore, basal-like tumors were associated with recurrence (p=0.023) as well as with metastasis (p=0.007) (Table V). However, using KRT stratification, we only could characterize 70% of cystectomy-treated patients, suggesting that other still unknown phenotypes may exist.

Table V – Clinicopathological information of luminal and basal-like tumors

		Luminal n (%)	**Basal-Like n (%)**	***p***
Stage	T2	9 (42.9)	5 (13.9)	0.014
	T3/T4	12 (57.1)	31 (86.1)	
Lymph-node metastasis	N_0	10 (76.9)	10 (47.6)	0.153
	N_1	3 (23.1)	11 (52.4)	
Recurrence	No	13 (76.5)	8 (36.4)	0.023
	Yes	4 (23.5)	14 (63.6)	
Metastasis formation	No	16 (76.2)	14 (38.9)	0.007
	Yes	5 (23.8)	22 (61.1)	

In order to evaluate the prognostic value of this stratification, Kaplan-Meier analysis was performed to estimate the behavior of bladder tumors from each subtype in terms of cancer-specific survival (CSS) and disease-free survival (DFS). We found that individuals whose tumors were classified as basal-like presented a decreased CSS when compared with the ones presenting luminal subtype tumors (mean 85 months *vs.*29 months; log rank, p=0.001, Fig. 7A). In terms of DFS the same could be observed (mean: 83 months *vs.*29 months; log rank, p=0.003; Fig.7B).

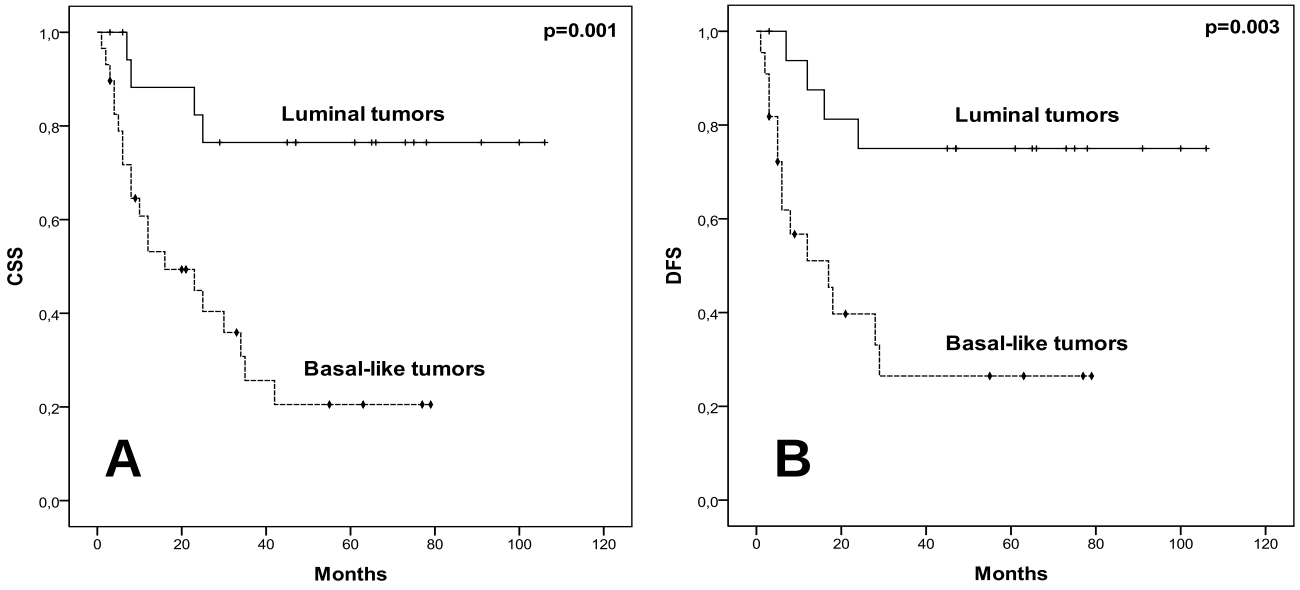
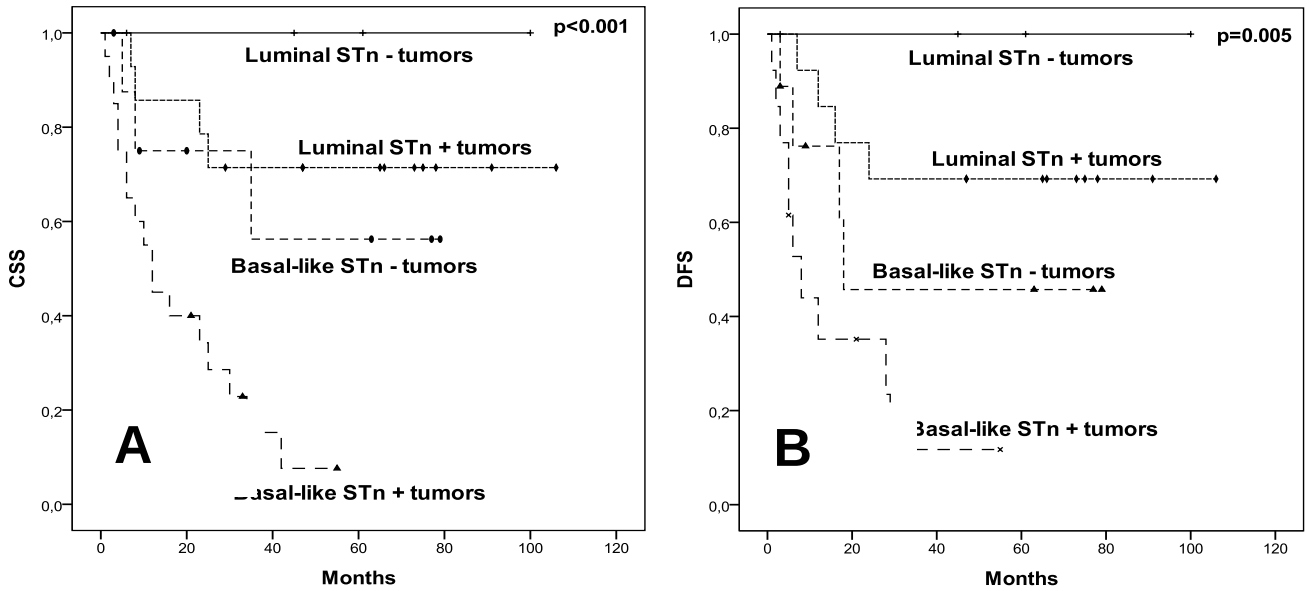


Figure 7 | Effect of bladder cancer subtypes in Cancer-specific survival (CSS) and Disease-free survival (DFS). Kaplan-Meier analysis to evaluate the association between (A) CSS and the basal-like and luminal subtypes and (B) DFS and the basal-like and luminal subtypes Comparison performed by log rank test **(A)** P 0.001 and **(B)** P 0.003. + censored luminal tumors; ♦ censored basal-like tumors.

To evaluate if STn could discriminate between basal-like and luminal tumors in terms of clinical outcome, a Kaplan-Meyer analysis was also performed. The results demonstrate that STn positive luminal tumors had similar CSS when compared to STn negative basal-like tumors (Fig.10A), Taking in consideration basal-like tumors, those had distinct CSS when STn expression was taking into the equation. As such, STn positive basal-like tumors had decreased CSS when compared to STn negative basal-like tumors (mean 53 months *vs.*19 months; log rank, p=0.028, Fig.8D). In relation to DFS, STn could also discriminate both basal-like and luminal tumors (Fig.8B).



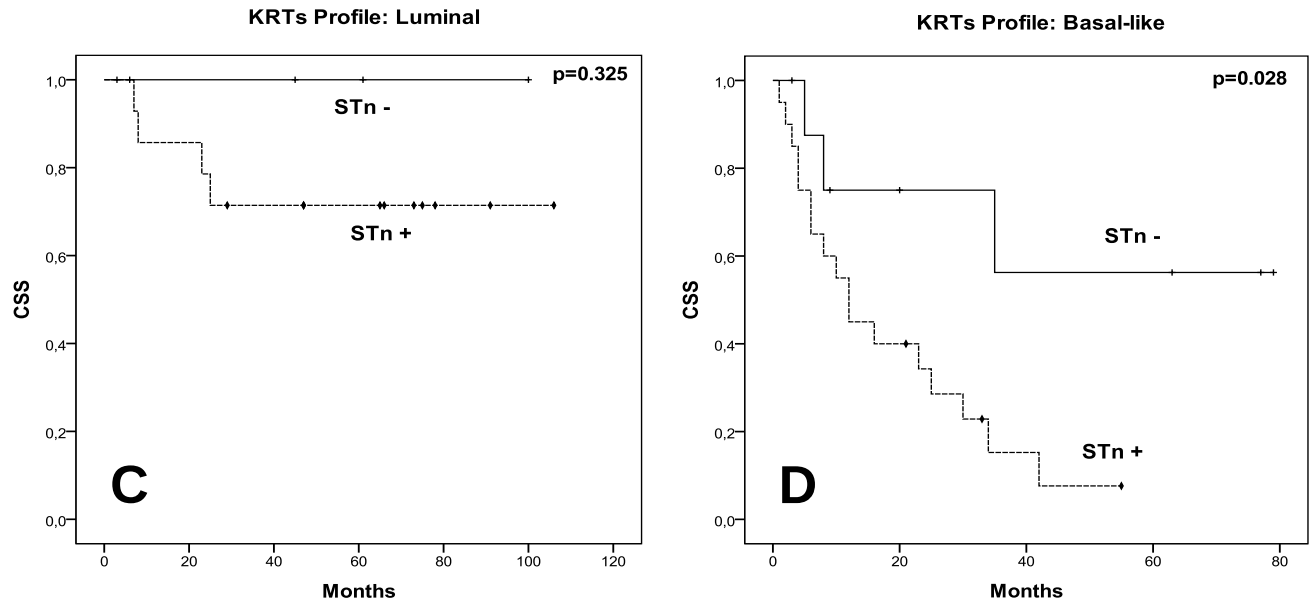


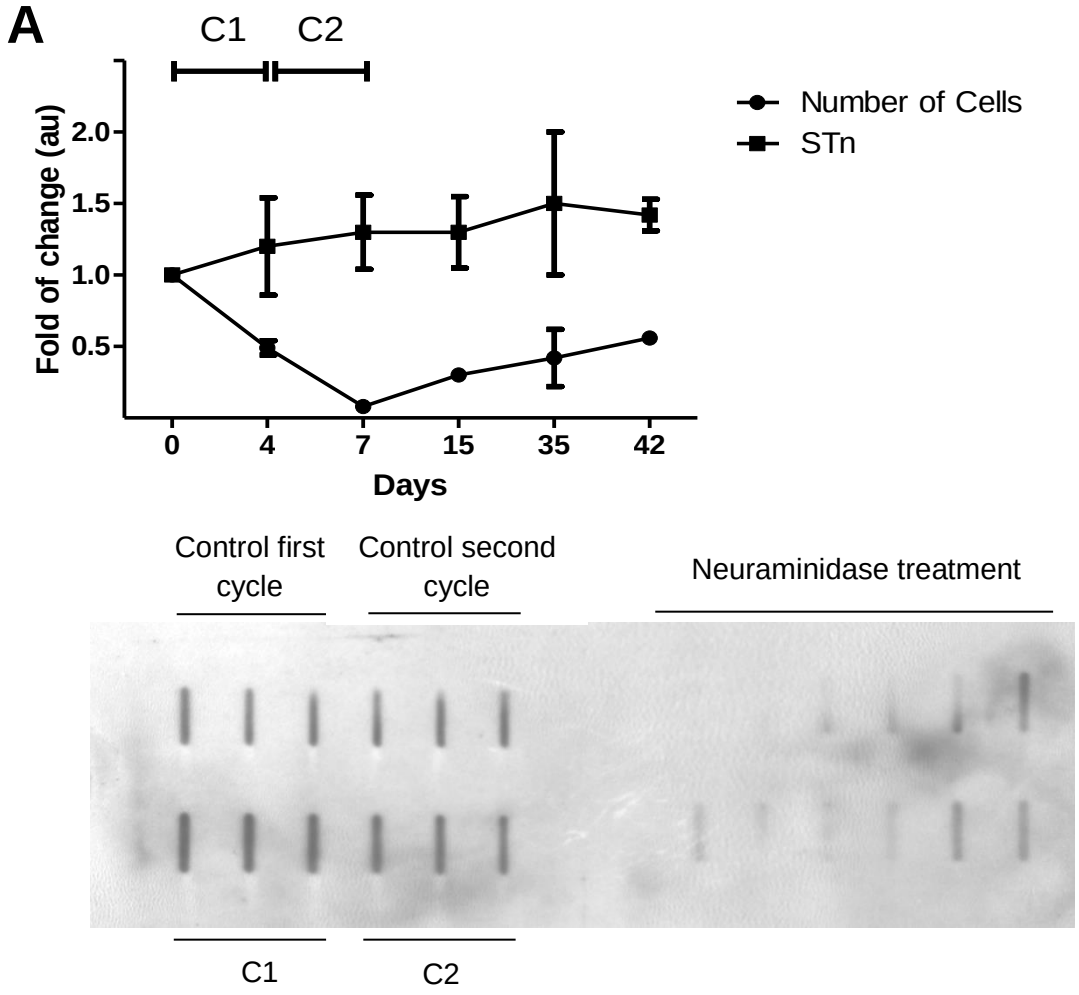
Figure 8 | Effect of STn immunoreactivity within bladder cancer subtypes in Cancer-specific survival (CSS) and Disease-free survival (DFS). Kaplan-Meier analysis to evaluate the association between **(A)** CSS and STn immunoreactivity within luminal, **(B)** basal-like and **(C)** both subtypes and **(D)** DFS and STn immunoreactivity within both subtypes. Comparison performed by log rank test **(A)** P<0.001 **(B)** P 0.005 **(C)** P 0.325 **(D)** 0.028. + censored STn negative tumors; ♦ censored STn positive tumors.

Classification of MIBC tumors submitted to chemotherapy according to KRT and STn expression patterns

Muscle-invasive tumors are usually treated with cisplatin-based chemotherapy before or after cystectomy in order to reduce the risk of metastasis. In order to better understand if KRTs or STn were relate with the outcome of patients that were submitted to chemotherapy, we evaluated its expression within tumors submitted to adjuvant and neo-adjuvant chemotherapy. However, STn and KRT stratification could not be used to subclassify patients in terms of response to treatment. Despite this, muscle-invasive tumors submitted to adjuvant chemotherapy had a high percentage of recurrence and progression and 70% of the metastasis stained for STn. Also, in spite of partial responses to neo-adjuvant chemotherapy, our results indicate that STn positive tumors before treatment maintained STn positivity when submitted to treatment. In addition it was observed an increase in the percentage of basal-like tumors after neo-adjuvant chemotherapy when compared with the initial TUR before chemotherapy (from 30 to 80% of cases).

Expression of STn in BC cells submitted to cisplatin treatment

T24 and HT1376 bladder cancer cells present a highly deddiferentiated and heterogeneous nature. To evaluate the presence of resistant clones, both cell lines were subjected to two consecutive exposures to IC50 concentrations of cisplatin, which is a common agent in bladder cancer treatment schemes. Treatment reduced the initial cell population in over 90% in both cell lines (Fig.9A and B); nevertheless the cells that resisted the second cycle were still viable. These were then allowed to expand for 30 days to disclose their capability to recover from treatment without further interventions. While some clones in T24 cells were capable of expanding during this period, HT1376 remained quiescent for a long period, after which the cells started to die. Contrasting with the significant decrease in cells following treatment, the levels of STn remained unchanged during treatments, suggesting the selection of STn-expressing clones. The specificity of the signal in the slot blots was confirmed by its disappearance after neuraminidase treatment.



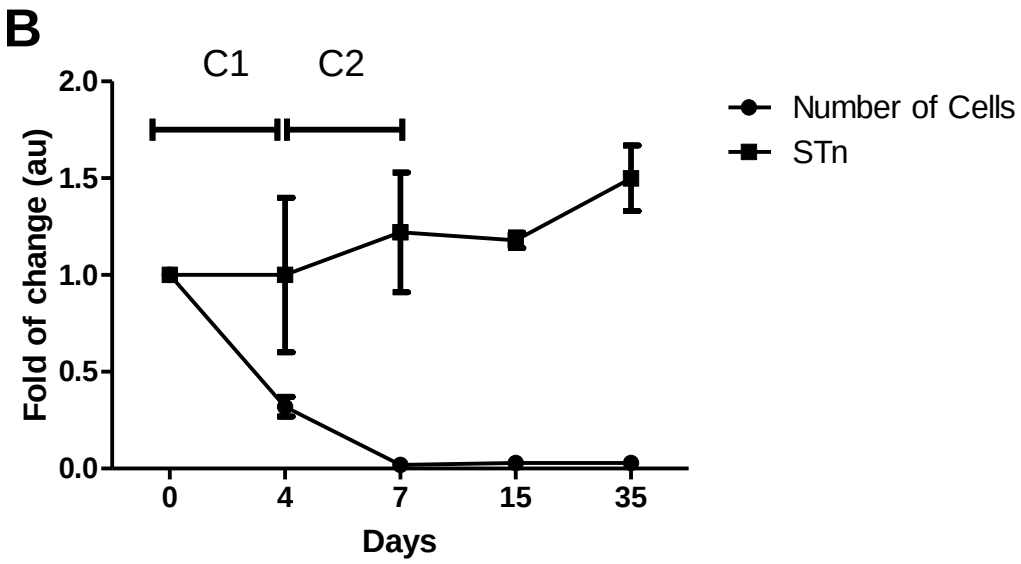


Figure 9 | STn expression in HT1376 and T24 cells exposed to Cisplatin. C1 and C2 represent the first and second cycles of cisplatin in **(A)** T24 and **(B)** HT1376 cell lines. Figure **(A)** also represents a nitrocellulose slot blot membrane incubated with TKH2 antigen without (left panel) and with (right panel) neuraminidase treatment. No significant difference was found between the two groups for STn expression. The decay of signal with neuraminidase treatment confirms signal specificity. Au: arnbitrary units.

Chemotherapy modulation of EMT and stemness

As previously described, EMT refers to a process in which epithelial cells reprogram and acquire mesenchymal traits such as motility and invasive properties in response to a defined set of extracellular stimuli. EMT has been implicated in therapeutic resistance and the generation of distant metastasis and both processes may be linked to the generation by EMT of CSCs. As such, T24 and HT1376 cells submitted to chemotherapy were characterized in relation to the expression of a panel of 21 genes associated with stem cell, epithelial, mesenchymal and EMT programs as exemplified on table V and its results are represented in Figure 10. In relation to HT1376 cells, these presented a significant up-regulation of KLF4 (stem), DSP, EPCAM (epithelial), FN1 (mesenchymal), RUNX1, SNAI1, TWIST1, ZEB2 (EMT) and down-regulation of CDH1 (epithelial), POUF5F1, SOX2 (stem cell), SPARC (cell shape) and VIM (mesenchymal). An integrative analysis of these differences using the software Cytoscape (Fig.11A) showed that HT1376 cell line presents a significant up-regulation of canonical Wnt signaling pathways and also a deregulation of cell-cell adhesion, translated by a negative regulation of cell-cell contact and adherent junction organization. Concerning T24 cell line, these presented up-regulation of CDH2 (mesenchymal), SNAI1, TWIST1 (EMT) and down-regulation of SNAI2 (EMT), CDH1

(epithelial) and LIN28A (stem). Again, an integrative analysis of these differences showed that T24 cell line presents a negative regulation of tight junction assembly and a negative regulation of DNA damage response signal transduction by a p53 class mediator (Fig.11B).

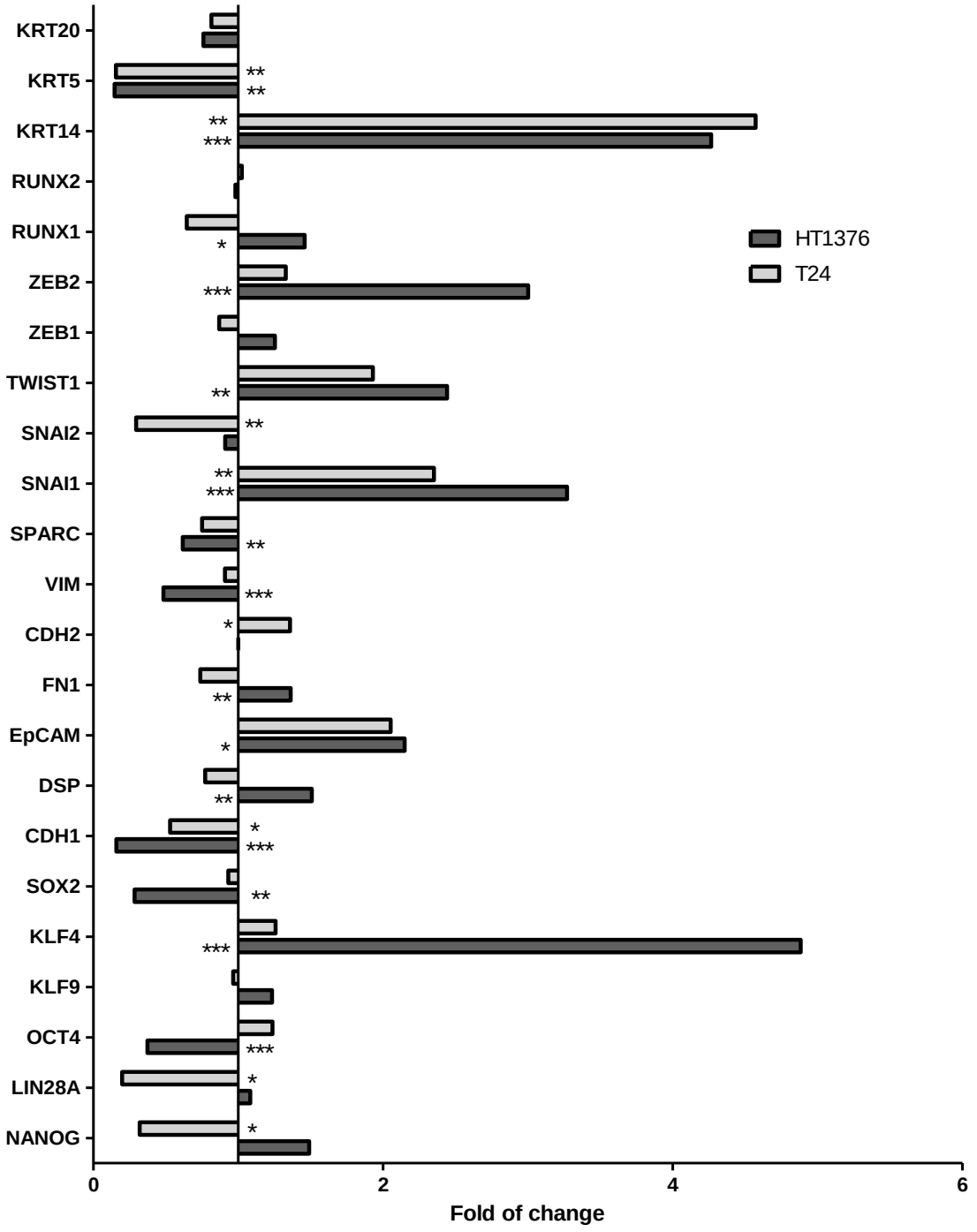


Figure 10 | Transcript levels of the analyzed genes for HT1376 and T24 cell lines.. Fold of increase for each analyzed gene. * p<0.05; ** p<0.01; *** p<0.001.

Chemotherapy modulation of KRT expression

In order to understand the differentiation patterns of cells submitted to chemotherapy, the KRT expression levels in T24 and HT1376 cells were also evaluated. Our results showed an up-regulation of KRT14 and a down-regulation of KRT5 for both cell lines (Fig.10). However, an integrative analysis of those was just possible in the HT1376 cell line (Fig.11A).

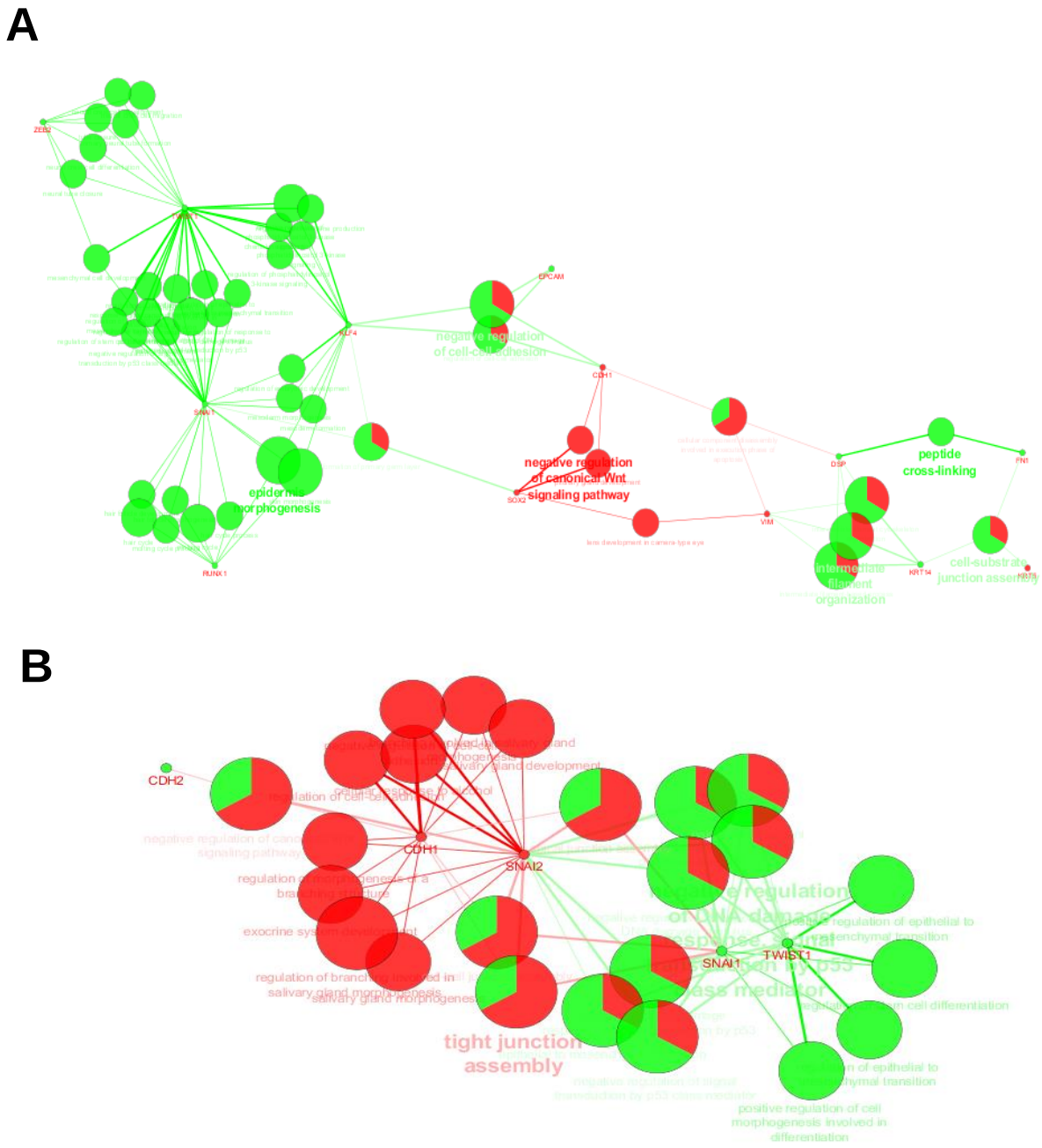


Figure 11 | Integrative gene expression data. The functional interaction network was obtained for **(A)** HT1376 and **(B)** T24 cell lines using Cytoscape Software Version 3.1.1.CluePedia and ClueGo plugins for single cluster analysis and comparison of gene clusters in order to explore cellular processes and their dynamics.

Discussion

In the past few years, some studies highlighted molecular profiling as a way of overcoming the clinical problems raised by BC heterogeneity [182, 186, 187]. These studies are based on disease subtyping using gene signatures which may help prognostication and prediction of response to treatment. Almost all of those studies revealed considerable overlapping on many of genes that define the subtypes. Keratins such as KRT5, 14 and 20 fulfill those criteria. KRTs follow the differentiation pattern of the three layers composing the urothelium and maintain the same pattern once malignant transformation occurs. As such, bladder tumors display keratin expression patterns that associate with tumor differentiation state.

Stratification of patients by BC subtypes using keratins showed significant prognostic utility and predictive value. Volkmer and colleagues proposed that the differential expression of keratin 14, 5 and 20 could help predicting three differentiation states: basal ($KRT14^{+}KRT5^{+}KRT20^{-}$), intermediate ($KRT14^{-}KRT5^{+}KRT20^{-}$), and differentiated ($KRT14^{-}KRT5^{-}KRT20^{+}$). Using this classification, basal tumors were highly related with worse overall survival [187]. In turn, Damrauer and colleagues defined two molecular subtypes the basal-like (high KRT14 and/or KRT5) and luminal (only high KRT20) subtypes [182]. Basal-like tumors, which include Volkmer´s basal and intermediate subtypes, were associated with worse overall survival. This discrepancy in terms of OS might be associated with not only the fact that Volkmer and colleagues evaluated NMIBC tumors in addition to MIBC tumors but also that half of the samples being classified as Intermediate subtype were non-muscle-invasive which have better prognosis. Other studies may also indicate potential predictive value. Cisplatin-based chemotherapy is only effective in 30-40% of cases and yet there´s no current available predictive factors able to identify patients who are likely to benefit from chemotherapy. Moreover, no effective alternative therapy has been identified for resistant tumors. Choi *et al.* defined three subtypes for muscle-invasive tumors: basal, luminal and p53-like subtypes. Basal and Luminal subtypes display similar KRT signatures as those found in *Volkmer et al*. while p53-like subtype was similar to that found in the intermediate subtype. However, the p53-like subgroup presented tumors that were resistant to cisplatin-based chemotherapy thus representing a subtype which might benefit from alternative therapies to overcome chemoresistance [188].

As clearly defined in the previous chapter as well as in other reports by our group, STn overexpression is associated with advanced stages of BC in addition to

many hallmarks of malignancy. As we just evaluated muscle invasive tumors, we hypothesized the introduction of STn into the subclassification proposed by Damrauer and colleagues in order to more accurately predict prognostic and predictive values.

Using the proposed classification, we could accurately characterize approximately 70% of the patients treated with radical cystectomy. This reflects the molecular heterogeneity within bladder tumors and suggests the need to improve on this KRT stratification. Our results indicate that basal-like tumors are associated with advanced stages of MIBC disease and, for the first time, we refer its association with recurrence as well as with the formation of metastasis. We also associated basal-like tumors with worse cancer-specific survival and disease-free survival. When STn was introduced in this model, basal-like tumors and even luminal tumors (despite not significantly) had worse cancer-specific survival than STn negative basal-like and luminal tumors. All of these facts denote a role of undifferentiated basal-like tumors in disease outcome and, for the first time, divide those tumors in two subgroups with distinct disease outcomes.

Concerning chemotherapy-treated patients, neither STn nor KRTs could be used to subdivide patients in terms of response to treatment. However in patients treated with adjuvant chemotherapy that denote treatment failure, recurrence and progression, 70% of those presented STn expression. Additionally, with regards to patients treated with neo-adjuvant chemotherapy, all of STn expressing ones before treatment maintained that phenotype when submitted to treatment. These results suggest the prevalence of STn on cells that resist to conventional chemotherapy. All of these observations are in accordance with Ferreira et al. [10] that suggested STn expression on quiescent areas of the tumor recognized as sites with high capacity in overcoming chemotherapy treatments. Altogether these findings suggest that STn expressing cells may constitute valuable targets to overcome chemoresistance

In order to understand the influence of cisplatin in BC cells *in vitro*, we submitted T24 and HT1376 cells to cisplatin in an IC50 concentration. It was shown that the STn expression did not vary significantly after treatment with cisplatin suggesting that the antigen is present on cells that resist to chemotherapy. In addition, these results are in accordance with clinical observations of patients submitted to neo-adjuvant chemotherapy which suggests STn as a suitable marker for guided therapeutics such as nano-encapsulated drugs that would improve drug delivery and reduce side effects.

To evaluate the characteristics of cells submitted to chemotherapy, we analyzed the gene expression status of a panel of 21 genes involved in stem cell, epithelial, mesenchymal and EMT programs. Our results demonstrated an up-regulation of genes

involved in EMT for both cell lines however most notably for HT1376 which demonstrate an enhanced capacity of migration and invasion capacities. An integrative analysis of the up and down-regulated genes for the HT1376 cell line revealed a positive regulation of canonical Wnt pathways and a negative regulation of cell-cell adhesion. These two evidences are a direct consequence of the down-regulation of the CDH1 gene which encodes for the E-cadherin protein. This molecule is responsible for cell-cell adhesion and its down-regulation displaces its interaction with β-catenin. Elevated levels of β-catenin enable this molecule to translocate to the nucleus and activate several genes among them those specifying EMT-inducing transcription factors. For the T24 cell, line the same integrative gene analysis showed a negative regulation of tight-junction assembly and a negative regulation of DNA damage response signal transduction by p53 class mediator. The first is closely related not only to the down-regulation of the CDH1 gene but also to the up-regulation of the CDH2 gene which encodes for N-dadherin. This dichotomy in terms of cadherins expression reveals the cadherin-switch, a process that usually happens when EMT programs are activated. This evidence reinforces the enhancement in migrating potential of cells submitted to chemotherapy. In relation to the second point, this reflects a characteristic of chemoresistant cells. These cells usually present an inhibition of p53-induced apoptosis which results in resistance to chemotherapy.

The expression levels of KRTs were also assessed and revealed an up-regulation of KRT14 and a down-regulation of KRT5 for both cell lines. As we know, KRT14 is associated with less differentiated tumors which mean that chemotherapy acts as a selector of less differentiated cells probably cells in the basal layer of the urothelium. It is also known that CSCs may reside in the basal-layer of the urothelium, a fact that sustains our hypothesis of the selection by chemotherapy of chemoresistant cells. Keratin analysis of FFPE tissues after neo-adjuvant chemotherapy also sustained these notions, as it was observed an increase in the basal-like signature after treatment when compared with TUR before chemotherapy.

In spite of these results, further studies are needed in order to evaluate if STn has a direct role in the induction of chemoresistance as well as if STn positive cells are able to form metastasis *in vivo* therefore recapitulating tumor heterogeneity.

Chapter IV | Glycoproteomic characterization of advanced bladder tumors

Abstract

In the previous chapter evidences have been presented supporting an association between STn expression and highly dedifferentiated advanced stage tumors and chemoresistant clones. As such, mining the STn-glycoproteome might be useful in terms of targeting those malignant phenotypes. This study applies a glycoproteomic approach to identify altered glycoproteins expressing STn in basal-like tumors that conserved STn expression after neoadjuvant chemotherapy. This glycoproteomic approach using nanoLC-ESI-MS/MS led to the identification of over 400 O-glycosites and 143 membrane STn-expressing glycoproteins that may be potential targets for targeted therapeutics. One of the glycoproteins identified was MUC16, a glycoprotein that has been reported in other tumors as well as in the serum of patients with BC but yet in bladder tumors. We have also found evidences of altered glycosylation in CD44, a cancer stem cell-associated glycoprotein in bladder cancer, which plays a key role in the mediation of invasion and disease dissemination. The expression of these glycoproteins was further validated in both primary tumors and the metastasis, and found conserved after neoadjuvant chemotherapy. These results not only validate previous observations by immunohistochemistry regarding STn expression in bladder tumors, but also provide a panel of abnormal O-glycosylated cell-surface proteins that may be used to selectively target more aggressive bladder tumors and ultimately improve BC management. More studies are now needed to fully disclose the biological and clinical significance of these alterations in bladder cancer.

Keywords: protein glycosylation, bladder cancer, sialyl-Tn, personalized biomarkers; chemoresistance; glycoproteome; mass spectrometry

Introduction

Glycosylation is one of the most prevalent, complex and tightly regulated posttranslational modification of cell-surface proteins, responsible by greatly expanding the variety of the human proteome. Particularly, O-GalNAc glycosylation which is regulated by several glycosyltransferases with distinct but overlapping specificities leads to a level of cell- and protein specific regulation. Recently, a precision mapping of

the human O-glycoproteome using the Simple Cell technology has revealed 6000 glycosites in more than 600 glycoproteins isolated from cancer cells of different origins, the majority of those found at the cell-surface. Furthermore it was found different cells express unique subsets of O-glycoproteins, providing evidences that the O-glycoproteome is differentially regulated and dynamic [189]. Moreover, it reinforces the need for specific mining of the glycoproteome for specific O-glycoforms.

In the two previous chapters sialyl-Tn was associated with worst cancer-specific survival in MIBC and possible plays a key role in resistance to chemotherapy. For the above mentioned reasons, sialyl-Tn might be an attractive biomarker for aggressive cellular phenotypes in BC. Nevertheless, nothing is known about STn-expressing proteins in BC, in contrast to other tumor types. Thus, this chapter devoted to identifying glycoproteins yielding STn, envisaging new insights about the role of this glycans in BC but also novel therapeutic targets.

Materials and Methods

Glycoprotein extraction and enrichment

Proteins were extracted from FFPE basal-like bladder tumors (KRT14+ and/or $KRT5^+$; $KRT20^-$) conserving STn expression after neoadjuvant chemotherapy, using Qproteome FFPE tissue kit (Qiagen) according to the suppliers instruction. The amount of protein in each extract was estimated with RC protein assay kit (BioRad). Thirty micrograms of protein were then separated by 4–16% gradient SDS–PAGE under reducing conditions, bands excised from the gels and proteins reduced, alkylated and digested *in situ* for MS analysis as described by Ferreira et al [190]. In addition, approximately 1mg of total protein resulting from pooling extracts from 5 tumors of male patients showing negative Tn and blood group A antigens were screened for STn-expressing glycoproteins. Briefly, the protein pool was subjected to neuraminidase treatment (10 U *Clostridium perfringens* neuraminidase Type VI (Sigma)) before loaded on 300 µl *Vicia villosa* agglutinin (VVA) agarose (Vector laboratories) column to enrich the extract in Tn-expressing glycoproteins. The column was then washed with 10 column volumes (CV) of 0.4 M Glucose in LAC A buffer (20 mM Tris-HCl pH 7.4, 150 mM NaCl, 1 M Urea, 1 mM $CaCl_2$, $MgCl_2$, $MnCl_2$, and $ZnCl_2$) followed by 1 ml 50 mM

NH_4HCO_3. The glycoproteins were then eluted by 4x 500 µl 0.05% RapiGest (Waters) with heating to 90°C for 10 min. The glycoprotein fraction was then directly reduced with 5 mM DTT (Sigma) for 40 min at 60˚C, alkylated with 10 mM iodoacetamide (Sigma) in dark for 45 min, and digested with trypsin (Promega).

nanoLC-ESI-MS/MS

A nanoLC system (Dionex, 3000 Ultimate nano-LC) was coupled on-line to a LTQ-Orbitrap XL mass spectrometer (Thermo Scientific) equipped with a nano-electrospray ion source (Thermo Scientific, EASY-Spray source). Eluent A was aqueous formic acid (0.2%) and eluent B was formic acid (0.2%) in acetonitrile. Samples (20 µl) were injected directly into a trapping column (C18 PepMap 100, 5 µm particle size) and washed over with an isocratic flux of 95% eluent A and 5% eluent B at a flow rate of 30 µl/min. After 3 minutes, the flux was redirected to the analytical column (EASY-Spray C18 PepMap, 100 Å, 150 mm x 75µm ID and 3 µm particle size) at a flow rate of 0.3 µl/min. Column temperature was set at 35º C. Peptide separation occurred using a linear gradient of 5–40% eluent B over 117 min., 50–90% eluent B over 5 min. and 5 min. with 90% eluent B. In order to favor the separation and identification of peptides presenting high hydrophobicity, samples were also analyzed with a two-step gradient protocol: 5–35% eluent B over 37 min., 35-65% eluent B over 80 min., followed by 65–90% eluent B over 5 min. and 5 min. with 90% buffer B.

The mass spectrometer was operated in the positive ion mode, with a spray voltage of 1.9 kV and a transfer capillary temperature of 250˚C. Tube lens voltage was set to 120 V. MS survey scans were acquired at an Orbitrap resolution of 60,000 for an *m/z* range from 300 to 2000. Tandem MS (MS/MS) data were acquired in the linear ion trap using a data dependent method with dynamic exclusion: The top 6 most intense ions were selected for collision induced dissociation (CID). CID settings were 35% normalized collision energy, 2 Da isolation window 30 ms activation time and an activation Q of 0.250. A window of 90 s was used for dynamic exclusion. Automatic Gain Control (AGC) was enabled and target values were 1.00e+6 for the Orbitrap and 1.00e+4 for LTQ MS^n analysis. Data were recorded with Xcalibur software version 2.1.

Data were analyzed automatically using the SequestHT search engine with the Percolator algorithm for validation of protein identifications (Proteome Discoverer 1.4, Thermo Scientific). Data were searched against the human proteome obtained from the SwissProt database on 22/11/2015, selecting trypsin as the enzyme and allowing for up to 2 missed cleavage sites a precursor ion mass tolerance of 10 ppm and 0.6 Da for

product ions. Carbamidomethylcysteine was selected as a fixed modification while oxidation of methionine (+15.99491), and modification of serine and threonine with HexNac (+203.07937 u) or HexNacNeuNac (Stn) (+494.17479) were defined as variable modifications. For whole tumor proteome analysis, only high confidence peptides were considered. In glycoproteomics studies, due to the high lability of the sugar moieties under CID conditions, and the consequent difficulty in identifying modified peptides, Sequest results of low confidence peptides were also considered. Protein grouping filters were thus set to consider PSMs with low confidence and ΔCn better than 0.05. The strict maximum parsimony principle was applied. A protein filter counting peptides only on top scored proteins was also set. Peptides were filtered for Xcorr ≥ 1.0 and ΔCn ≤ 0.05. Cytoplasm membrane proteins with at least 1 annotated glycosylation site were selected and the modifications were validated manually. Membrane proteins were sorted using NetOGlyc version 4.0 (http://www.cbs.dtu.dk/services/NetOGlyc/) to generate the final protein list. Protein molecular and biological functions were interpreted using Panther [191].

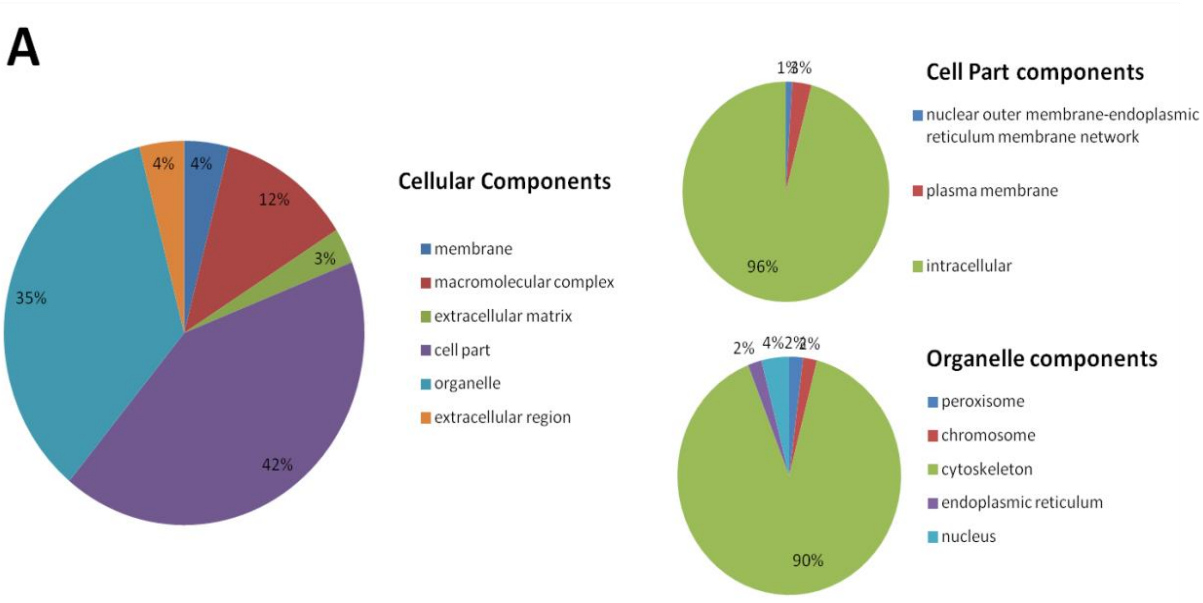
Immunohistochemistry

Prior to MS analysis FFPE tissues were screened for the Tn antigen (conditions used described in the chapter 1) and for blood group A determinants (Monoclonal Mouse anti-human anti-blood group A antigen; clone HE-195) at a dilution of 1:100 in PBS, after 1h incubation at 37°C). Bladder tumors and metastasis were also screened for MUC-16 (Monoclonal Rabbit Anti-Human Anti-CA-125 antibody; Clone EPR1020(2); Abcam) at a dilution of 1:100 in PBS, overnight incubation at 37°C and for CD44 (Monoclonal Mouse Anti-Human anti-CD44 antibody; clone 156-3C11; Cell Signaling) at a dilution 1:100 in PBS, 1h incubation at 37°C. Technique procedures according to the previous sections.

Results

Mapping the STn-glycoproteome is crucial to develop highly specific targeted therapeutics against chemoresistant cells. However, while the majority of glycoproteomics studies presented so far have focused mostly on bodily fluids and, to lower extent, human tissues, none has attempted to address protein glycosylation in FFPE tissues. Herein, as a proof of concept, we have used a commercial kit from QIAGEN to extract proteins from basal-like tumors conserving STn expression after neoadjuvant chemotherapy. Prior to protein extraction, tissue sections were screen by immunohistochemistry for Tn and blood group A expression and negative cases were elected for downstream glycoproteomics studies.

Conventional gel-based and nanoLC-MS/MS proteomics methods led to the identification of 2578 peptides corresponding to 294 of the most abundant proteins in these tumors, thereby illustrating the feasibility of using FFPE has starting material for retrospective proteomic studies (Appendix B). Gene ontology interpretation of the results using Panther highlighted the presence of proteins from all cell compartments, including plasma membrane proteins (4%; Fig. 12A); nevertheless an overrepresentation of cytoplasmatic and cytoskeleton proteins could be observed (Fig. 12A). Main represented molecular functions included binding, structural and catalytical activities, whereas main molecular functions were set on metabolic and cellular processes (Fig. 12B).



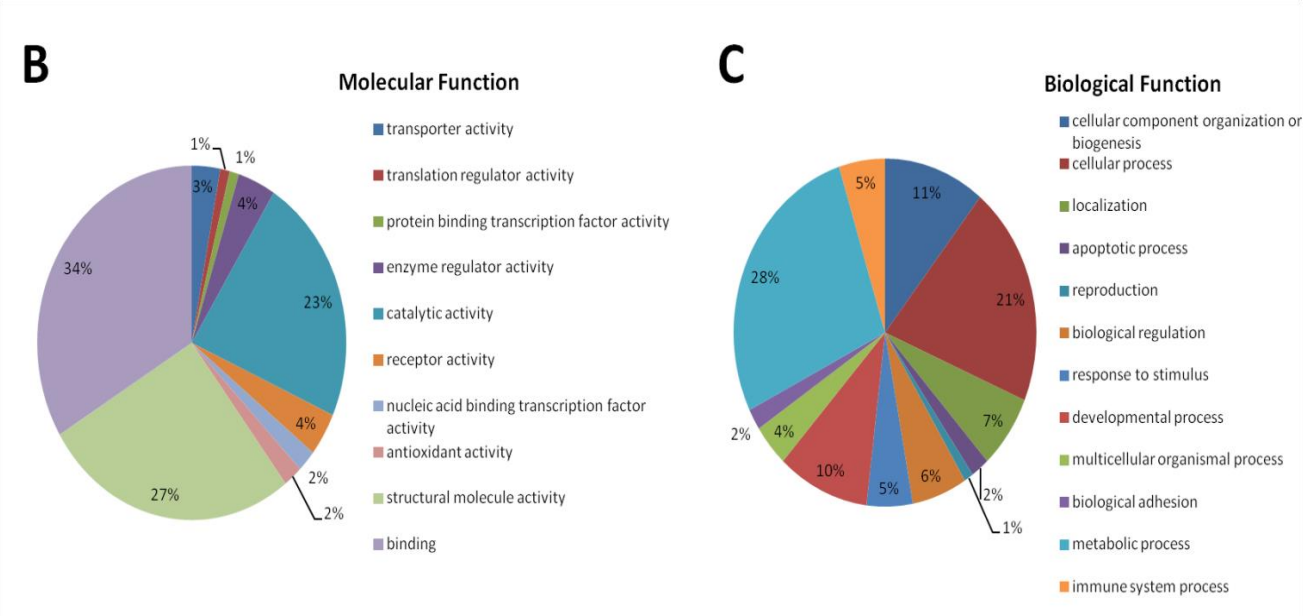


Figure 12 | Gene ontology interpretation of the identified proteins using Panther. Graphical overview of the percentage of the identified proteins within **(A)** each cellular component and its association with **(B)** molecular and **(C)** biological functions.

The extracts were then digested with a α-neuraminidase to remove sialic acids from STn-expressing glycoproteins exposing the Tn antigen. This allowed the introduction of an enrichment step based on affinity to *Vicia villosa* lectin that selectively binds terminal GalNAc residues. The absence of Tn and blood group A determinants in these chosen cases ensured the specificity of the enrichment for STn-expressing proteins. Subsequent nanoLC-MS/MS analysis led to the identification of over 400 O-glycosites and 143 membrane STn-expressing glycoproteins that may be potential targets for targeted therapeutics. Interestingly, STn-expressing proteins were found to be associated with a wide array of molecular and biological functions as depicted in detail in Figure 13. In particular STn-expressing proteins mostly mediate binding to other proteins and participate in hydrolase catalytic activities. STn-expressing proteins also mediate cellular processes involved with cell communication, in particular cell-cell signaling, and regulation of several biological events, namely primary metabolic processes. These observations provide key preliminary insights to understand the role of STn expression in bladder cancer.

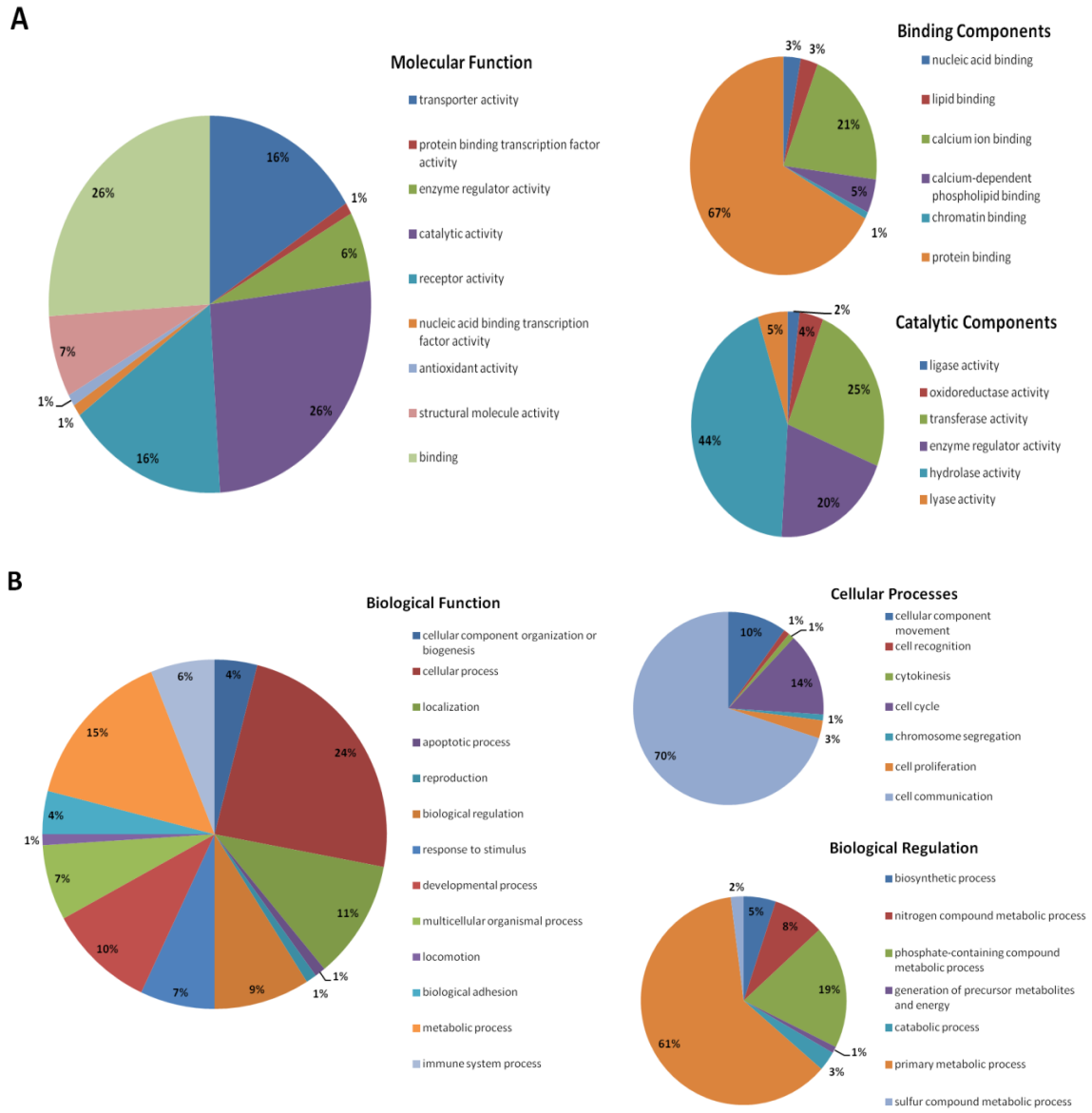


Figure 15 | Gene ontology interpretation of the identified STn-expressing proteins using Panther. Graphical overview of the percentage of identified proteins associated with its **(A)** molecular and **(B)** biological functions.

The obtained protein list (Appendix C) was then interpreted using the STITCH software that provides interaction networks of chemicals and proteins [192]. This exploratory bioinformatics tool highlighted, for cisplatin and gemcibatine which were used for bladder cancer treatment, a protein hub with EGRF. Even though EGFR was not included in our final list of abnormally O-glycosylated proteins, this protein contains, according to NetOGlyc 4.0, 19 putative O-glycosites that should be carefully analyzed in future studies. Nevertheless, a downstream association was observed between

EGFR and CD44, a typical bladder cancer stem-cell associated glycoprotein also associated with drug resistant phenotypes [193, 194] (Fig.14), could be observed. More importantly, the CD44 protein was also frequently associated with tumors of the basal-like phenotype and consequently poor prognosis [182]. The present glycoproteomics study allowed the unambiguous assignment of one abnormally glycosylated peptide common to the CD44 splice variants 3 and 4 (Fig.15). More studies should now be conducted to fully map CD44 O-glycosites in the context of chemoresistance, disclose the nature of the splice variants associated with advanced stage disease and the clinical implications of these observations.

As discussed in detail in the introduction section, altered O-glycosylation in cancer is often associated to the overexpression of mucins. Accordingly, this study led to the identification of MUC16 as one of the major carriers for STn in advanced stage bladder tumors. Even though no associations were found between MUC16 and resistance cisplatin and/or gemcitabine, this is the first time this glycoprotein is being described in bladder cancer. Given the key role of MUC16 in cancer progression in other solid tumors, namely ovarian carcinomas [195], future studies should also be conducted to address the clinical significance of these observations.

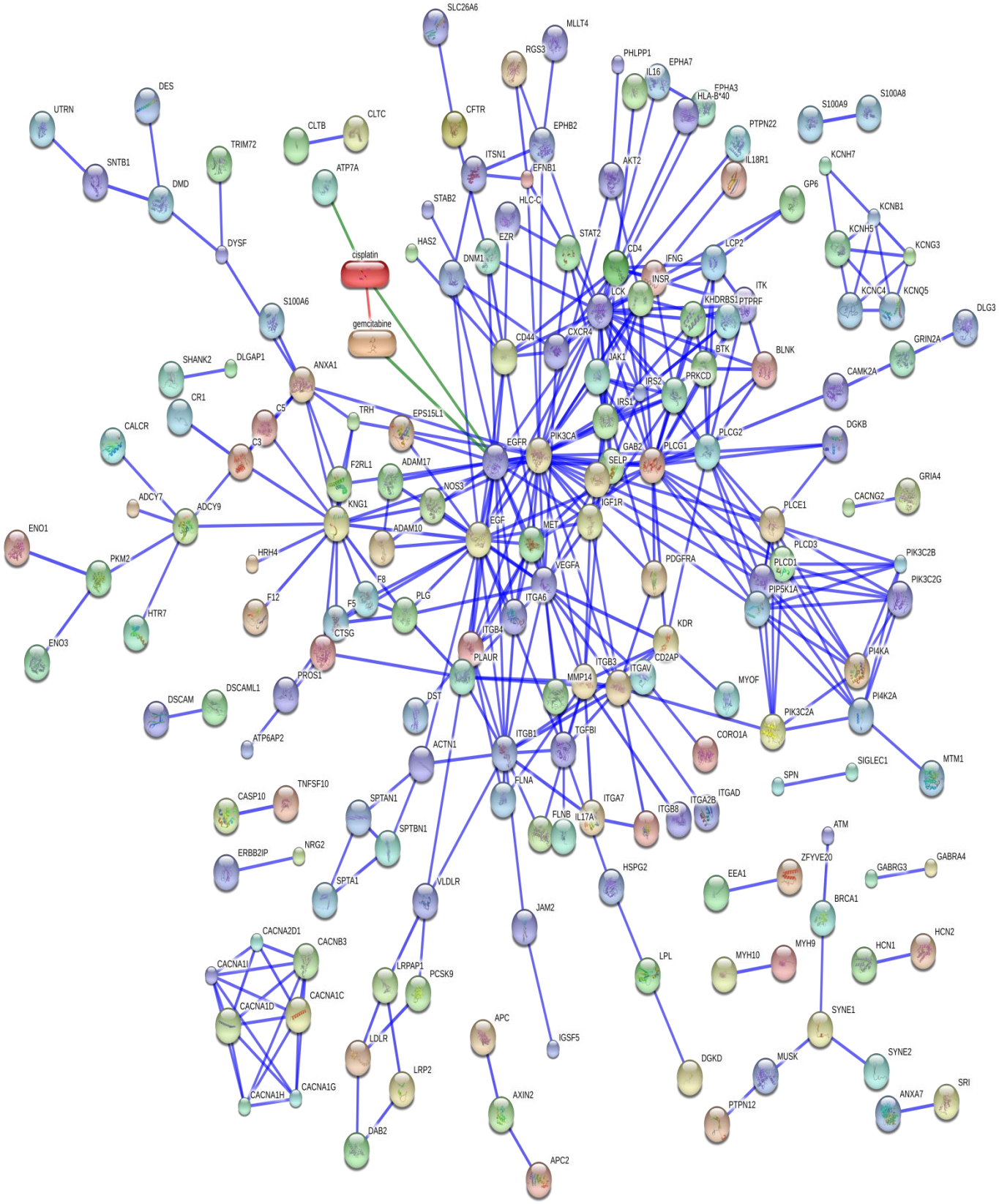


Figure 14 | **Study of the interaction networks between cisplatin and gemcitabine and the obtained protein list using STITCH.**

#1	a*	a*-HexNAc	a²⁺	a²⁺-HexNAc	a³⁺	b*	b²⁺	b²⁺-HexNAc	b³⁺	Seq.	x*	x²⁺	x²⁺-HexNAc	x³⁺	x³⁺-HexNAc	y*	y²⁺	y²⁺-HexNAc	y³⁺	#2
1										E(387)										23
2										D					745.33		1206.04		804.36	22
3										S			1059.98							21
4						469.17				H		1117.99						1003.47	737.01	20
5	528.20									S		1049.47		699.98	632.29					19
6										T										18
7	730.30		365.65			758.29				T				637.29						17
8										G			803.37							16
9									373.82	T(395)-HexNAc							863.40			15
10		959.41	581.75	480.217		1190.48				A				483.22			711.34		474.56	14
11				515.73						A		688.81								13
12	1304.56									A										12
13								608.76		S										11
14					488.22					A						1121.53	561.27			10
15			800.35							H				359.49						9
16										T		470.21								8
17								806.85		S						812.38				7
18							976.92			H	751.33									6
19			1011.44	909.91	674.63					P										5
20			1076.96		718.31					M	517.22									4
21										Q										3
22					780.00					G										2
23										R(409)										1

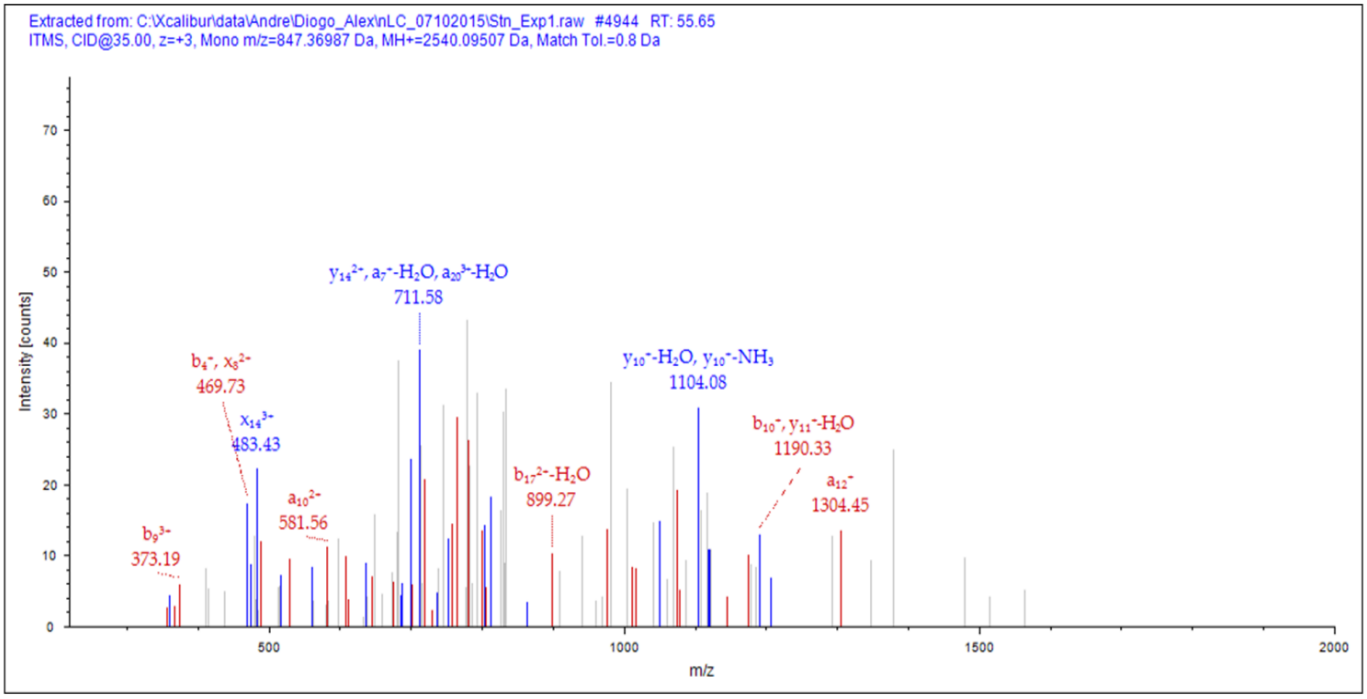


Figure 15 | MS/MS main fragment ions for the abnormally O-glycosylated CD44 glycopeptides. Based on the fragment ions presented in the upper table and the corresponding annotate MS/MS spectra (lower Figure) it was possible to unequivocally assign a GalNAc residue to the T395 on the glycopeptides chain.

Expression of STn-MUC16 and STn-CD44 in bladder tumors

Given the key role of CD44 and MUC16 in cancer, subsequent studies were conducted to determine their expression in the context of chemotherapy response,

based on the evaluation of human tumors before and after (neo)adjuvant chemotherapy. An immunohistochemistry analysis of consecutive bladder tumor sections revealed that STn (Fig. 16A/C), MUC-16 (Fig.16B) and CD44 (Fig.16D) expressions were conserved after neo-adjuvant chemotherapy. Furthermore, the expression of the two glycoproteins co-localized with the STn in all of the cases. Likewise, STn-positive metastases were also positive for MUC-16, CD44 and a co-localization between glycoproteins and the glycan was also observed (data not shown). Future studies should be conducted to validate these findings in a larger number of cases to disclose the biomarker value of these abnormally glycosylated proteins in the context of bladder cancer.

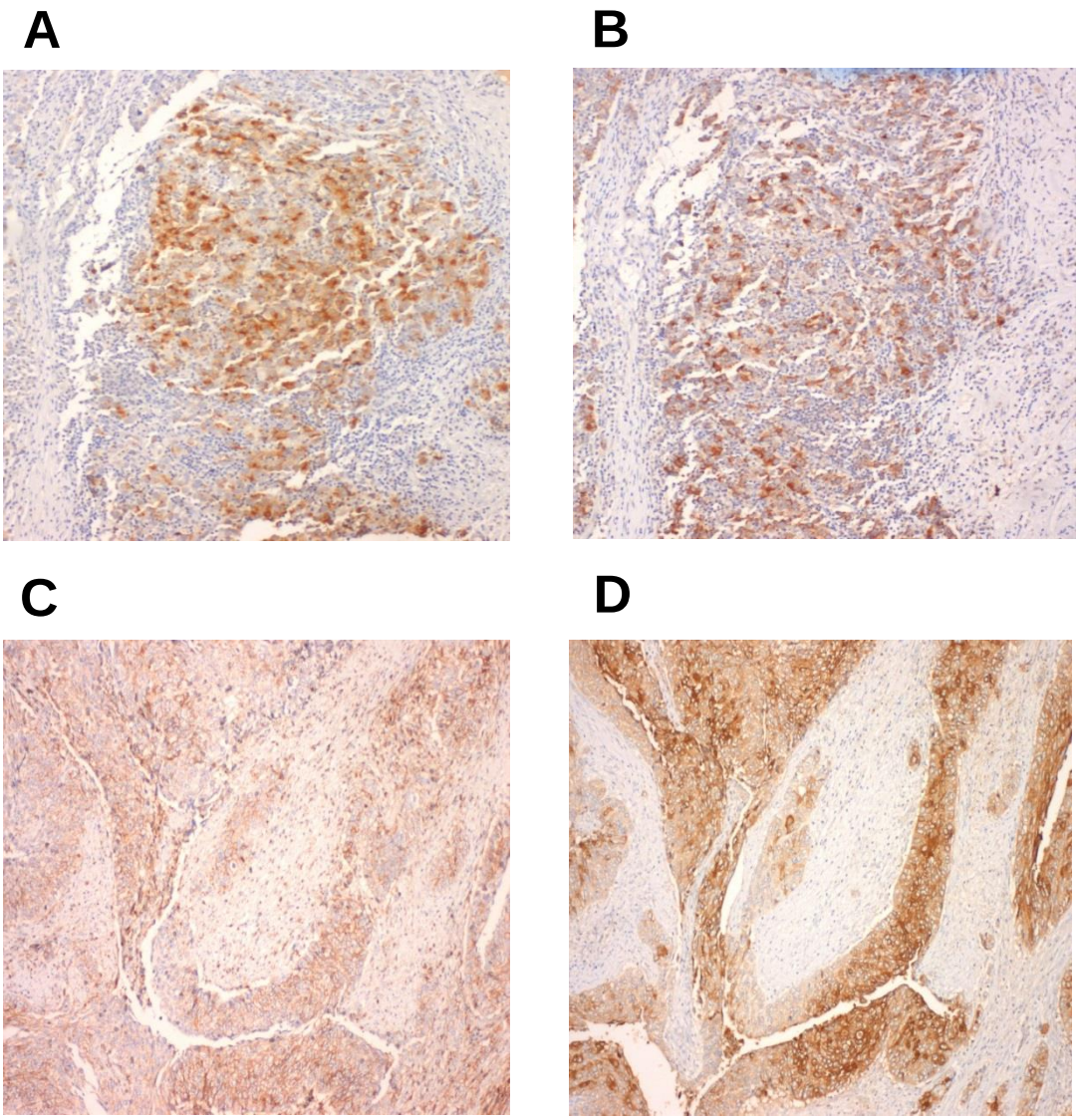


Figure 16 | Immunohistochemical validation of the identified glycoproteins on primary bladder tumors (x100). **C**omparative expression between (A) STn and (B) MUC-16 and between (C) STn and (D) CD44 corresponding in sequential section of the same tumor.

Discussion

The STn antigen is considered a biomarker associated with malignant phenotypes, aggressiveness, metastasis and poor prognosis in MIBC. STn might also be associated with chemoresistance as indicated by our previous findings. This malignant signature suggests that the identification of the STn-expressing glycoproteins may improve our knowledge about the role of this type of glycosylation in BC as well as provide new insights about novel therapeutics towards chemoresistant cells.

All proteomic studies addressing cancer chemoresistance presented to this date have used mostly cell lines as starting models. Moreover, very few have analyzed tumor tissues and none used formalin fixed paraffin embedded samples, which are frequently part of any hospital's archives. Herein the feasibility of this approach was demonstrated, opening a new analytical strategy for retrospective proteomics studies on well characterized tumor sections. Moreover it may facilitate associations with long-term clinical variables such as survival, which are not possible to establish in studies involving the prospective collections of fresh tumors.

Using this strategy it was possible to identify about 400 O-glycosites and 143 membrane-bound proteins expressing STn namely CD44 and MUC-16. CD44 glycoprotein is the receptor for hyaluronic acid (HA) and mediates cell-cell and cell-matrix interactions through its affinity with HA and possibly other ligands such as MMPs. Several reports associate CD44 with cisplatin resistance in many types of cancer [58, 196, 197]. For instance, in head and neck squamous cell carcinoma, HA-CD44 interaction leads to the activation of multiple cell-signaling pathways that result in cisplatin resistance. After HA-CD44 interaction recruits and forms a CD44-EGFR-LARG multimolecular complex, multiple downstream signaling pathways are activated; cross-talk among Ras, RhoA, ROK, and PI-3 kinase can occur, promoting diverse head and neck cancer progression behaviors and chemoresistance [197]. Other studies also reported alterations in the glycophenotype of CSCs of different tissue origins compared to other cancer cells [198]. CD44 appears to naturally express STn [199] and appears to be a marker of CSCs in BC [69, 193]. As such, knowing the glycosylation machinery of chemoresistant CSCs may provide new insights towards more specific targeted therapy.

Concerning MUC16, no connection has been described between cisplatin and this glycoprotein. This glycoprotein is thought to provide a protective, lubricating barrier

against particles and infectious agents at mucosal surfaces and has a role in cancer by promoting cancer cell proliferation and inhibiting anti-cancer immune responses [195]. We found this glycoprotein in our series of bladder tumors and metastasis denoting a role in response to treatment and bladder carcinogenesis. Moreover, MUC16 have been used as diagnostic marker of ovarian cancer (CA-125 test) [195] and its appearance in the serum of patients with BC suggested its presence in bladder tumors [200],

Further validation of the identified glycoproteins in BC tissues revealed its presence in both primary tumors and metastasis and found conserved after neo-adjuvant chemotherapy. These facts also reinforce previous observations regarding STn expression in bladder tumors. However, further confirmation of these results using Proximity Ligation Assay as well as attending the clinical and biological significance of these alterations in BC is warranted.

Chapter V | Concluding remarks and future perspectives

Sialyl-Tn is considered a pan-carcinoma antigen. Despite absent or weakly expressed by fetal and normal adult tissues, STn is expressed in approximately 80% of all human carcinomas and in all cases is associated with adverse outcome and worst overall-survival. In agreement with this, our group concluded that approximately 70% of high-grade bladder tumors express STn. Moreover, its appearance correlated with enhanced motility and invasive potential of cancer cells *in vitro,* EMT, protection from host immune responses, impairment of DC maturation and promoter of a tolerogenic function, Now, and in a wide array of BC specimens, we also associated STn with metastasis as well as an independent prognostic marker of worst CSS.

Concerning MIBC and metastatic disease, surgery and cisplatin-based (neo)adjuvant chemotherapy regimens are the only available therapeutic option. Despite frequent initial treatment responses, overall survival does not exceed 12–16 months in metastatic patients therefore urging the introduction of novel targeted therapeutics. Even though efficient against the tumor bulk, non-proliferative chemoresistant areas of the tumor characterized by the presence of clones that are responsible for disease relapse, progression and dissemination remains a major concern. Previous results from our group suggest that these chemoresistant areas express STn. Herein; our results demonstrate that STn expression levels persist after two cycles of cisplatin in T24 and HT1376 UC cell lines that mirror two of the main pathways of invasion in bladder cancer. Gene expression analysis of these chemoresistant cells showed activated EMT programs, positive regulation of canonical Wnt signaling pathways and negative regulation of cell-cell adhesion for the HT1376 cell line and a negative regulation of both tight-junction assembly and DNA damage response signal transduction by p53 class mediator in the T24 cell line. This demonstrates the capability of chemoresistant cells in migrating and disseminating as well as evading apoptosis in response to DNA damage.

We also found that keratin profiling might be useful in patient stratification and prognosis. As such, we found that basal-like tumors had worse CSS than luminal tumors. The introduction of STn in this model improved the predictive capacity of this model by allowing sorting patients at higher risk of disease progression in two groups. Moreover, STn was present in the metastasis of 70% of patients that had disease progression after adjuvant chemotherapy. Additionally, STn positive patients that underwent neo-adjuvant chemotherapy maintained their STn positivity after treatment which is in accordance with *in vitro* results.

Gene expression analysis of keratins in FFPE tissues of patients treated with neo-adjuvant chemotherapy revealed an increase in the basal-like signature after chemotherapy when compared with TUR before chemotherapy. Also, in cell lines submitted to cisplatin, an over-expression of KRT14 and down-regulation of KRT5 revealed that chemotherapy possibly acts as a selector of less differentiated cells in the tumor.

Taking in consideration the association between STn and chemoresistance, mapping the STn-glycoproteome is crucial to develop highly specific targeted therapeutics against chemoresistant cells. In a glycoproteomic approach in a set of FFPE tissues conserving STn expression after neo-adjuvant chemotherapy, we identified about 300 of the most abundant proteins of the tumors under study which illustrate the feasibility of using FFPE has starting material for retrospective proteomic studies. In relation to STn-expressing proteins, 400 O-glycosites and 143 proteins were identified. From these, the most relevant identified proteins were MUC16 and CD44. MUC-16 has been identified in the serum of patients with BC but yet in bladder tumors while CD44 is a known stem-cell marker in BC involved in invasion and disease dissemination. This approach has identified, for the first time, a panel of abnormal O-glycosylated cell-surface proteins that may be used to selectively target more aggressive bladder tumors and ultimately improve BC management.

Further studies should be aimed to understand the biological and clinical significance of the identified glycoproteins in BC. It is also imperative to understand if STn has a direct role in promoting chemoresistance and also if STn positive cells are able to form metastasis and recapitulate tumor heterogeneity in distant locations. Moreover, it will be important to fully disclose the cancer-specific nature of the abnormally glycosylated-forms of MUC16 and CD44 and its expression in preneoplastic lesions. A careful mapping of the glycome on these proteins in the context of chemoresitance as well as the development of specific ligands is also warranted envisaging highly specific cancer therapeutics.

References

1. Ferlay, J., et al., *Estimates of worldwide burden of cancer in 2008: GLOBOCAN 2008.* Int J Cancer, 2010. **127**(12): p. 2893-917.
2. Goodison, S., C.J. Rosser, and V. Urquidi, *Bladder cancer detection and monitoring: assessment of urine- and blood-based marker tests.* Mol Diagn Ther, 2013. **17**(2): p. 71-84.
3. Knowles, M.A. and C.D. Hurst, *Molecular biology of bladder cancer: new insights into pathogenesis and clinical diversity.* Nat Rev Cancer, 2015. **15**(1): p. 25-41.
4. Burger, M., et al., *Epidemiology and risk factors of urothelial bladder cancer.* Eur Urol, 2013. **63**(2): p. 234-41.
5. Babjuk, M., et al., *EAU guidelines on non-muscle-invasive urothelial carcinoma of the bladder: update 2013.* Eur Urol, 2013. **64**(4): p. 639-53.
6. Witjes, J.A., et al., *EAU guidelines on muscle-invasive and metastatic bladder cancer: summary of the 2013 guidelines.* Eur Urol, 2014. **65**(4): p. 778-92.
7. Bellmunt, J., et al., *Bladder cancer: ESMO Practice Guidelines for diagnosis, treatment and follow-up.* Ann Oncol, 2014. **25 Suppl 3**: p. iii40-8.
8. Hussain, M.H., et al., *Bladder cancer: narrowing the gap between evidence and practice.* J Clin Oncol, 2009. **27**(34): p. 5680-4.
9. Sievert, K.D., et al., *Economic aspects of bladder cancer: what are the benefits and costs?* World J Urol, 2009. **27**(3): p. 295-300.
10. Ferreira, J.A., et al., *Overexpression of tumour-associated carbohydrate antigen sialyl-Tn in advanced bladder tumours.* Mol Oncol, 2013. **7**(3): p. 719-31.
11. Freitas, D.P., et al., *Therapy-induced enrichment of putative lung cancer stem-like cells.* Int J Cancer, 2014. **134**(6): p. 1270-8.
12. Cui, Y., et al., *Drug resistance and ATP-dependent conjugate transport mediated by the apical multidrug resistance protein, MRP2, permanently expressed in human and canine cells.* Mol Pharmacol, 1999. **55**(5): p. 929-37.
13. Taniguchi, K., et al., *A human canalicular multispecific organic anion transporter (cMOAT) gene is overexpressed in cisplatin-resistant human cancer cell lines with decreased drug accumulation.* Cancer Res, 1996. **56**(18): p. 4124-9.
14. Kobayashi, T., et al., *Possible mechanism responsible for the acquisition of resistance to cis-diamminedichloroplatinum (II) by cultured human testicular seminoma cells.* J Urol, 2004. **171**(5): p. 1929-33.
15. Tada, Y., et al., *MDR1 gene overexpression and altered degree of methylation at the promoter region in bladder cancer during chemotherapeutic treatment.* Clin Cancer Res, 2000. **6**(12): p. 4618-27.
16. Hoffmann, A.C., et al., *MDR1 and ERCC1 expression predict outcome of patients with locally advanced bladder cancer receiving adjuvant chemotherapy.* Neoplasia, 2010. **12**(8): p. 628-36.
17. Knipp, M., *Metallothioneins and platinum(II) anti-tumor compounds.* Curr Med Chem, 2009. **16**(5): p. 522-37.
18. Siegsmund, M.J., et al., *Cisplatin-resistant bladder carcinoma cells: enhanced expression of metallothioneins.* Urol Res, 1999. **27**(3): p. 157-63.
19. Wülfing, C., et al., *Metallothionein in bladder cancer: correlation of overexpression with poor outcome after chemotherapy.* World J Urol, 2007. **25**(2): p. 199-205.

20. Satoh, M., et al., *Modulation of resistance to anticancer drugs by inhibition of metallothionein synthesis.* Cancer Res, 1994. **54**(20): p. 5255-7.
21. Ishikawa, T., C.D. Wright, and H. Ishizuka, *GS-X pump is functionally overexpressed in cis-diamminedichloroplatinum (II)-resistant human leukemia HL-60 cells and down-regulated by cell differentiation.* J Biol Chem, 1994. **269**(46): p. 29085-93.
22. Chen, H.H., et al., *Elevated glutathione levels confer cellular sensitization to cisplatin toxicity by up-regulation of copper transporter hCtr1.* Mol Pharmacol, 2008. **74**(3): p. 697-704.
23. Bedford, P., et al., *Factors influencing the sensitivity of two human bladder carcinoma cell lines to cis-diamminedichloroplatinum(II).* Chem Biol Interact, 1987. **61**(1): p. 1-15.
24. Byun, S.S., et al., *Augmentation of cisplatin sensitivity in cisplatin-resistant human bladder cancer cells by modulating glutathione concentrations and glutathione-related enzyme activities.* BJU Int, 2005. **95**(7): p. 1086-90.
25. Yokomizo, A., et al., *Cellular levels of thioredoxin associated with drug sensitivity to cisplatin, mitomycin C, doxorubicin, and etoposide.* Cancer Res, 1995. **55**(19): p. 4293-6.
26. Takahara, P.M., et al., *Crystal structure of double-stranded DNA containing the major adduct of the anticancer drug cisplatin.* Nature, 1995. **377**(6550): p. 649-52.
27. Bellmunt, J., et al., *Gene expression of ERCC1 as a novel prognostic marker in advanced bladder cancer patients receiving cisplatin-based chemotherapy.* Ann Oncol, 2007. **18**(3): p. 522-8.
28. Kawashima, A., et al., *Excision repair cross-complementing group 1 may predict the efficacy of chemoradiation therapy for muscle-invasive bladder cancer.* Clin Cancer Res, 2011. **17**(8): p. 2561-9.
29. Usanova, S., et al., *Cisplatin sensitivity of testis tumour cells is due to deficiency in interstrand-crosslink repair and low ERCC1-XPF expression.* Mol Cancer, 2010. **9**: p. 248.
30. Chen, Z., et al., *Attenuated expression of xeroderma pigmentosum group C is associated with critical events in human bladder cancer carcinogenesis and progression.* Cancer Res, 2007. **67**(10): p. 4578-85.
31. Xu, X.S., et al., *Histone deacetylases (HDACs) in XPC gene silencing and bladder cancer.* J Hematol Oncol, 2011. **4**: p. 17.
32. Catto, J.W., et al., *Differential expression of hMLH1 and hMSH2 is related to bladder cancer grade, stage and prognosis but not microsatellite instability.* Int J Cancer, 2003. **105**(4): p. 484-90.
33. Konstantakou, E.G., et al., *Human bladder cancer cells undergo cisplatin-induced apoptosis that is associated with p53-dependent and p53-independent responses.* Int J Oncol, 2009. **35**(2): p. 401-16.
34. Hong, J.H., et al., *Antisense Bcl2 oligonucleotide in cisplatin-resistant bladder cancer cell lines.* BJU Int, 2002. **90**(1): p. 113-7.
35. Bolenz, C., et al., *Optimizing chemotherapy for transitional cell carcinoma by application of bcl-2 and bcl-xL antisense oligodeoxynucleotides.* Urol Oncol, 2007. **25**(6): p. 476-82.
36. Cho, H.J., et al., *Upregulation of Bcl-2 is associated with cisplatin-resistance via inhibition of Bax translocation in human bladder cancer cells.* Cancer Lett, 2006. **237**(1): p. 56-66.
37. Miyake, H., et al., *Overexpression of Bcl-2 in bladder cancer cells inhibits apoptosis induced by cisplatin and adenoviral-mediated p53 gene transfer.* Oncogene, 1998. **16**(7): p. 933-43.
38. Cooke, P.W., et al., *Bcl-2 expression identifies patients with advanced bladder cancer treated by radiotherapy who benefit from neoadjuvant chemotherapy.* BJU Int, 2000. **85**(7): p. 829-35.

39. Kim, J.K., et al., *Up-regulation of Bfl-1/A1 via NF-kappaB activation in cisplatin-resistant human bladder cancer cell line.* Cancer Lett, 2004. **212**(1): p. 61-70.
40. Bilim, V., et al., *Role of XIAP in the malignant phenotype of transitional cell cancer (TCC) and therapeutic activity of XIAP antisense oligonucleotides against multidrug-resistant TCC in vitro.* Int J Cancer, 2003. **103**(1): p. 29-37.
41. Pinho, M.B., et al., *XAF1 mRNA expression improves progression-free and overall survival for patients with advanced bladder cancer treated with neoadjuvant chemotherapy.* Urol Oncol, 2009. **27**(4): p. 382-90.
42. Mizutani, Y., Y. Katsuoka, and B. Bonavida, *Prognostic significance of second mitochondria-derived activator of caspase (Smac/DIABLO) expression in bladder cancer and target for therapy.* Int J Oncol, 2010. **37**(2): p. 503-8.
43. Lee, E.K., et al., *A Smac mimetic augments the response of urothelial cancer cells to gemcitabine and cisplatin.* Cancer Biol Ther, 2013. **14**(9): p. 812-22.
44. Yang, D., et al., *Therapeutic potential of siRNA-mediated combined knockdown of the IAP genes (Livin, XIAP, and Survivin) on human bladder cancer T24 cells.* Acta Biochim Biophys Sin (Shanghai), 2010. **42**(2): p. 137-44.
45. Als, A.B., et al., *Emmprin and survivin predict response and survival following cisplatin-containing chemotherapy in patients with advanced bladder cancer.* Clin Cancer Res, 2007. **13**(15 Pt 1): p. 4407-14.
46. Mizutani, Y., et al., *Enhanced sensitivity of bladder cancer cells to tumor necrosis factor related apoptosis inducing ligand mediated apoptosis by cisplatin and carboplatin.* J Urol, 2001. **165**(1): p. 263-70.
47. Mizutani, Y., O. Yoshida, and B. Bonavida, *Sensitization of human bladder cancer cells to Fas-mediated cytotoxicity by cis-diamminedichloroplatinum (II).* J Urol, 1998. **160**(2): p. 561-70.
48. Wu, X.X. and Y. Kakehi, *Enhancement of lexatumumab-induced apoptosis in human solid cancer cells by Cisplatin in caspase-dependent manner.* Clin Cancer Res, 2009. **15**(6): p. 2039-47.
49. Lee, S., et al., *The role of c-FLIP in cisplatin resistance of human bladder cancer cells.* J Urol, 2013. **189**(6): p. 2327-34.
50. Oren, M., *Decision making by p53: life, death and cancer.* Cell Death Differ, 2003. **10**(4): p. 431-42.
51. Vekris, A., et al., *Molecular determinants of the cytotoxicity of platinum compounds: the contribution of in silico research.* Cancer Res, 2004. **64**(1): p. 356-62.
52. Kigawa, J., et al., *Effect of p53 gene transfer and cisplatin in a peritonitis carcinomatosa model with p53-deficient ovarian cancer cells.* Gynecol Oncol, 2002. **84**(2): p. 210-5.
53. Kanamori, Y., et al., *A newly developed adenovirus-mediated transfer of a wild-type p53 gene increases sensitivity to cis-diamminedichloroplatinum (II) in p53-deleted ovarian cancer cells.* Eur J Cancer, 1998. **34**(11): p. 1802-6.
54. Shirakawa, T., et al., *Drug-resistant human bladder-cancer cells are more sensitive to adenovirus-mediated wild-type p53 gene therapy compared to drug-sensitive cells.* Int J Cancer, 2001. **94**(2): p. 282-9.
55. Nishiyama, H., J. Watanabe, and O. Ogawa, *p53 and chemosensitivity in bladder cancer.* Int J Clin Oncol, 2008. **13**(4): p. 282-6.
56. Cote, R.J., et al., *p53 and treatment of bladder cancer.* Nature, 1997. **385**(6612): p. 123-5.
57. Qureshi, K.N., et al., *TP53 accumulation predicts improved survival in patients resistant to systemic cisplatin-based chemotherapy for muscle-invasive bladder cancer.* Clin Cancer Res, 1999. **5**(11): p. 3500-7.
58. Barr, M.P., et al., *Generation and characterisation of cisplatin-resistant non-small cell lung cancer cell lines displaying a stem-like signature.* PLoS One, 2013. **8**(1): p. e54193.

59. Ma, L., et al., *Cancer stem-like cells can be isolated with drug selection in human ovarian cancer cell line SKOV3.* Acta Biochim Biophys Sin (Shanghai), 2010. **42**(9): p. 593-602.
60. Hayashi, S., et al., *Lin28a is a putative factor in regulating cancer stem cell-like properties in side population cells of oral squamous cell carcinoma.* Exp Cell Res, 2013. **319**(8): p. 1220-8.
61. Zhang, Y., et al., *Cancer stem-like cells contribute to cisplatin resistance and progression in bladder cancer.* Cancer Lett, 2012. **322**(1): p. 70-7.
62. Falso, M.J., B.A. Buchholz, and R.W. White, *Stem-like cells in bladder cancer cell lines with differential sensitivity to cisplatin.* Anticancer Res, 2012. **32**(3): p. 733-8.
63. Enderling, H., L. Hlatky, and P. Hahnfeldt, *Cancer Stem Cells: A Minor Cancer Subpopulation that Redefines Global Cancer Features.* Front Oncol, 2013. **3**: p. 76.
64. Moore, N. and S. Lyle, *Quiescent, slow-cycling stem cell populations in cancer: a review of the evidence and discussion of significance.* J Oncol, 2011. **2011**.
65. Gaisa, N.T., et al., *The human urothelium consists of multiple clonal units, each maintained by a stem cell.* J Pathol, 2011. **225**(2): p. 163-71.
66. Kurzrock, E.A., et al., *Label-retaining cells of the bladder: candidate urothelial stem cells.* Am J Physiol Renal Physiol, 2008. **294**(6): p. F1415-21.
67. He, X., et al., *Differentiation of a highly tumorigenic basal cell compartment in urothelial carcinoma.* Stem Cells, 2009. **27**(7): p. 1487-95.
68. Castillo-Martin, M., et al., *Molecular pathways of urothelial development and bladder tumorigenesis.* Urol Oncol, 2010. **28**(4): p. 401-8.
69. Chan, K.S., et al., *Identification, molecular characterization, clinical prognosis, and therapeutic targeting of human bladder tumor-initiating cells.* Proc Natl Acad Sci U S A, 2009. **106**(33): p. 14016-21.
70. Ning, Z.F., et al., *Subpopulations of stem-like cells in side population cells from the human bladder transitional cell cancer cell line T24.* J Int Med Res, 2009. **37**(3): p. 621-30.
71. She, J.J., et al., *Identification of side population cells from bladder cancer cells by DyeCycle Violet staining.* Cancer Biol Ther, 2008. **7**(10): p. 1663-8.
72. Brandt, W.D., et al., *Urothelial carcinoma: stem cells on the edge.* Cancer Metastasis Rev, 2009. **28**(3-4): p. 291-304.
73. Alison, M.R., S.M. Lim, and L.J. Nicholson, *Cancer stem cells: problems for therapy?* J Pathol, 2011. **223**(2): p. 147-61.
74. Soltanian, S. and M.M. Matin, *Cancer stem cells and cancer therapy.* Tumour Biol, 2011. **32**(3): p. 425-40.
75. Yang, Y.M. and J.W. Chang, *Bladder cancer initiating cells (BCICs) are among EMA-CD44v6+ subset: novel methods for isolating undetermined cancer stem (initiating) cells.* Cancer Invest, 2008. **26**(7): p. 725-33.
76. Klatte, T., et al., *Absent CD44v6 expression is an independent predictor of poor urothelial bladder cancer outcome.* J Urol, 2010. **183**(6): p. 2403-8.
77. Huang, P., et al., *Cancer stem cell-like characteristics of a CD133(+) subpopulation in the J82 human bladder cancer cell line.* Mol Clin Oncol, 2013. **1**(1): p. 180-184.
78. Su, Y., et al., *Aldehyde dehydrogenase 1 A1-positive cell population is enriched in tumor-initiating cells and associated with progression of bladder cancer.* Cancer Epidemiol Biomarkers Prev, 2010. **19**(2): p. 327-37.
79. Jinesh, G.G., et al., *Blebbishields, the emergency program for cancer stem cells: sphere formation and tumorigenesis after apoptosis.* Cell Death Differ, 2013. **20**(3): p. 382-95.
80. Bentivegna, A., et al., *Biological heterogeneity of putative bladder cancer stem-like cell populations from human bladder transitional cell carcinoma samples.* Cancer Sci, 2010. **101**(2): p. 416-24.

81. Fletcher, J.I., et al., *ABC transporters in cancer: more than just drug efflux pumps.* Nat Rev Cancer, 2010. **10**(2): p. 147-56.
82. McConkey, D.J., et al., *Role of epithelial-to-mesenchymal transition (EMT) in drug sensitivity and metastasis in bladder cancer.* Cancer Metastasis Rev, 2009. **28**(3-4): p. 335-44.
83. Baumgart, E., et al., *Identification and prognostic significance of an epithelial-mesenchymal transition expression profile in human bladder tumors.* Clin Cancer Res, 2007. **13**(6): p. 1685-94.
84. Yun, S.J. and W.J. Kim, *Role of the epithelial-mesenchymal transition in bladder cancer: from prognosis to therapeutic target.* Korean J Urol, 2013. **54**(10): p. 645-50.
85. Mani, S.A., et al., *The epithelial-mesenchymal transition generates cells with properties of stem cells.* Cell, 2008. **133**(4): p. 704-15.
86. Morel, A.P., et al., *Generation of breast cancer stem cells through epithelial-mesenchymal transition.* PLoS One, 2008. **3**(8): p. e2888.
87. Polyak, K. and R.A. Weinberg, *Transitions between epithelial and mesenchymal states: acquisition of malignant and stem cell traits.* Nat Rev Cancer, 2009. **9**(4): p. 265-73.
88. Brabletz, T., et al., *Opinion: migrating cancer stem cells - an integrated concept of malignant tumour progression.* Nat Rev Cancer, 2005. **5**(9): p. 744-9.
89. Ju, T. and R.D. Cummings, *A unique molecular chaperone Cosmc required for activity of the mammalian core 1 beta 3-galactosyltransferase.* Proc Natl Acad Sci U S A, 2002. **99**(26): p. 16613-8.
90. Torres, C.R. and G.W. Hart, *Topography and polypeptide distribution of terminal N-acetylglucosamine residues on the surfaces of intact lymphocytes. Evidence for O-linked GlcNAc.* J Biol Chem, 1984. **259**(5): p. 3308-17.
91. Bektas, M. and D.S. Rubenstein, *The role of intracellular protein O-glycosylation in cell adhesion and disease.* J Biomed Res, 2011. **25**(4): p. 227-36.
92. Dall'Olio, F., et al., *Mechanisms of cancer-associated glycosylation changes.* Front Biosci (Landmark Ed), 2012. **17**: p. 670-99.
93. Kudelka, M.R., et al., *Simple sugars to complex disease--mucin-type O-glycans in cancer.* Adv Cancer Res, 2015. **126**: p. 53-135.
94. Marcos, N.T., et al., *ST6GalNAc-I controls expression of sialyl-Tn antigen in gastrointestinal tissues.* Front Biosci (Elite Ed), 2011. **3**: p. 1443-55.
95. Pinho, S., et al., *Biological significance of cancer-associated sialyl-Tn antigen: modulation of malignant phenotype in gastric carcinoma cells.* Cancer Lett, 2007. **249**(2): p. 157-70.
96. Itzkowitz, S.H., et al., *Expression of Tn, sialosyl-Tn, and T antigens in human colon cancer.* Cancer Res, 1989. **49**(1): p. 197-204.
97. Cazet, A., et al., *Tumour-associated carbohydrate antigens in breast cancer.* Breast Cancer Res, 2010. **12**(3): p. 204.
98. Itzkowitz, S., et al., *Expression of Tn, sialosyl Tn, and T antigens in human pancreas.* Gastroenterology, 1991. **100**(6): p. 1691-700.
99. Ricardo, S., et al., *Detection of glyco-mucin profiles improves specificity of MUC16 and MUC1 biomarkers in ovarian serous tumours.* Mol Oncol, 2015. **9**(2): p. 503-12.
100. Ju, T., et al., *Tn and sialyl-Tn antigens, aberrant O-glycomics as human disease markers.* Proteomics Clin Appl, 2013. **7**(9-10): p. 618-31.
101. Julien, S., P.A. Videira, and P. Delannoy, *Sialyl-tn in cancer: (how) did we miss the target?* Biomolecules, 2012. **2**(4): p. 435-66.
102. Nakagoe, T., et al., *Predictive factors for preoperative serum levels of sialy Lewis(x), sialyl Lewis(a) and sialyl Tn antigens in gastric cancer patients.* Anticancer Res, 2002. **22**(1A): p. 451-8.

103. Nakagoe, T., et al., *Pre-operative serum levels of sialyl Tn antigen predict liver metastasis and poor prognosis in patients with gastric cancer.* Eur J Surg Oncol, 2001. **27**(8): p. 731-9.
104. Nakagoe, T., et al., *Circulating sialyl Lewis(x), sialyl Lewis(a), and sialyl Tn antigens in colorectal cancer patients: multivariate analysis of predictive factors for serum antigen levels.* J Gastroenterol, 2001. **36**(3): p. 166-72.
105. Davidson, B., et al., *Carbohydrate antigen expression in primary tumors, metastatic lesions, and serous effusions from patients diagnosed with epithelial ovarian carcinoma: evidence of up-regulated Tn and Sialyl Tn antigen expression in effusions.* Hum Pathol, 2000. **31**(9): p. 1081-7.
106. Ogata, S., P.J. Maimonis, and S.H. Itzkowitz, *Mucins bearing the cancer-associated sialosyl-Tn antigen mediate inhibition of natural killer cell cytotoxicity.* Cancer Res, 1992. **52**(17): p. 4741-6.
107. Ju, T., et al., *Human tumor antigens Tn and sialyl Tn arise from mutations in Cosmc.* Cancer Res, 2008. **68**(6): p. 1636-46.
108. Julien, S., et al., *Sialyl-Tn vaccine induces antibody-mediated tumour protection in a relevant murine model.* Br J Cancer, 2009. **100**(11): p. 1746-54.
109. Miles, D., et al., *Phase III multicenter clinical trial of the sialyl-TN (STn)-keyhole limpet hemocyanin (KLH) vaccine for metastatic breast cancer.* Oncologist, 2011. **16**(8): p. 1092-100.
110. Pinho, S.S. and C.A. Reis, *Glycosylation in cancer: mechanisms and clinical implications.* Nat Rev Cancer, 2015. **15**(9): p. 540-55.
111. Chia, D., et al., *Use of monoclonal antibodies to sialylated Lewisx and sialylated Lewisa for serological tests of cancer.* Cancer Res, 1985. **45**(1): p. 435-7.
112. Reis, C.A., et al., *Alterations in glycosylation as biomarkers for cancer detection.* J Clin Pathol, 2010. **63**(4): p. 322-9.
113. Berg, E.L., et al., *A carbohydrate domain common to both sialyl Le(a) and sialyl Le(X) is recognized by the endothelial cell leukocyte adhesion molecule ELAM-1.* J Biol Chem, 1991. **266**(23): p. 14869-72.
114. Läubli, H. and L. Borsig, *Selectins promote tumor metastasis.* Semin Cancer Biol, 2010. **20**(3): p. 169-77.
115. Paschos, K.A., D. Canovas, and N.C. Bird, *The engagement of selectins and their ligands in colorectal cancer liver metastases.* J Cell Mol Med, 2010. **14**(1-2): p. 165-74.
116. Mathieu, S., et al., *Introducing alpha(1,2)-linked fucose into hepatocarcinoma cells inhibits vasculogenesis and tumor growth.* Int J Cancer, 2007. **121**(8): p. 1680-9.
117. Kannagi, R., *Carbohydrate antigen sialyl Lewis a--its pathophysiological significance and induction mechanism in cancer progression.* Chang Gung Med J, 2007. **30**(3): p. 189-209.
118. Malagolini, N., et al., *Biosynthesis and expression of the Sda and sialyl Lewis x antigens in normal and cancer colon.* Glycobiology, 2007. **17**(7): p. 688-97.
119. Izawa, M., et al., *Expression of sialyl 6-sulfo Lewis X is inversely correlated with conventional sialyl Lewis X expression in human colorectal cancer.* Cancer Res, 2000. **60**(5): p. 1410-6.
120. Robbe-Masselot, C., et al., *Expression of a core 3 disialyl-Le(x) hexasaccharide in human colorectal cancers: a potential marker of malignant transformation in colon.* J Proteome Res, 2009. **8**(2): p. 702-11.
121. Fukasawa, T., et al., *Associated expression of α2,3sialylated type 2 chain structures with lymph node metastasis in distal colorectal cancer.* Surg Today, 2013. **43**(2): p. 155-62.
122. Hebbar, M., et al., *Prognostic value of tumoral sialyltransferase expression and circulating E-selectin concentrations in node-negative breast cancer patients.* Int J Biol Markers, 2003. **18**(2): p. 116-22.

123. Dall'Olio, F. and M. Chiricolo, *Sialyltransferases in cancer.* Glycoconj J, 2001. **18**(11-12): p. 841-50.
124. Lise, M., et al., *Clinical correlations of alpha2,6-sialyltransferase expression in colorectal cancer patients.* Hybridoma, 2000. **19**(4): p. 281-6.
125. Jun, L., et al., *Altered mRNA expressions of sialyltransferases in human gastric cancer tissues.* Med Oncol, 2012. **29**(1): p. 84-90.
126. Petretti, T., et al., *Altered mRNA expression of glycosyltransferases in human colorectal carcinomas and liver metastases.* Gut, 2000. **46**(3): p. 359-66.
127. Dall'Olio, F., N. Malagolini, and F. Serafini-Cessi, *Enhanced CMP-NeuAc:Gal beta 1,4GlcNAc-R alpha 2,6 sialyltransferase activity of human colon cancer xenografts in athymic nude mice and of xenograft-derived cell lines.* Int J Cancer, 1992. **50**(2): p. 325-30.
128. Chiricolo, M., et al., *Phenotypic changes induced by expression of beta-galactoside alpha2,6 sialyltransferase I in the human colon cancer cell line SW948.* Glycobiology, 2006. **16**(2): p. 146-54.
129. Yamamoto, H., et al., *Alpha2,6-sialylation of cell-surface N-glycans inhibits glioma formation in vivo.* Cancer Res, 2001. **61**(18): p. 6822-9.
130. Seales, E.C., et al., *Hypersialylation of beta1 integrins, observed in colon adenocarcinoma, may contribute to cancer progression by up-regulating cell motility.* Cancer Res, 2005. **65**(11): p. 4645-52.
131. Christie, D.R., et al., *ST6Gal-I expression in ovarian cancer cells promotes an invasive phenotype by altering integrin glycosylation and function.* J Ovarian Res, 2008. **1**(1): p. 3.
132. Zhuo, Y. and S.L. Bellis, *Emerging role of alpha2,6-sialic acid as a negative regulator of galectin binding and function.* J Biol Chem, 2011. **286**(8): p. 5935-41.
133. Zhuo, Y., R. Chammas, and S.L. Bellis, *Sialylation of beta1 integrins blocks cell adhesion to galectin-3 and protects cells against galectin-3-induced apoptosis.* J Biol Chem, 2008. **283**(32): p. 22177-85.
134. Falconer, R.A., et al., *Polysialyltransferase: a new target in metastatic cancer.* Curr Cancer Drug Targets, 2012. **12**(8): p. 925-39.
135. Tanaka, F., et al., *Prognostic significance of polysialic acid expression in resected non-small cell lung cancer.* Cancer Res, 2001. **61**(4): p. 1666-70.
136. Potapenko, I.O., et al., *Glycan gene expression signatures in normal and malignant breast tissue; possible role in diagnosis and progression.* Mol Oncol, 2010. **4**(2): p. 98-118.
137. Liu, Y.C., et al., *Sialylation and fucosylation of epidermal growth factor receptor suppress its dimerization and activation in lung cancer cells.* Proc Natl Acad Sci U S A, 2011. **108**(28): p. 11332-7.
138. Blomme, B., et al., *Alteration of protein glycosylation in liver diseases.* J Hepatol, 2009. **50**(3): p. 592-603.
139. Miyoshi, E., K. Moriwaki, and T. Nakagawa, *Biological function of fucosylation in cancer biology.* J Biochem, 2008. **143**(6): p. 725-9.
140. Hiller, K.M., et al., *Transfection of alpha(1,3)fucosyltransferase antisense sequences impairs the proliferative and tumorigenic ability of human colon carcinoma cells.* Mol Carcinog, 2000. **27**(4): p. 280-8.
141. Yin, X., et al., *Knockdown of fucosyltransferase III disrupts the adhesion of circulating cancer cells to E-selectin without affecting hematopoietic cell adhesion.* Carbohydr Res, 2010. **345**(16): p. 2334-42.
142. Pérez-Garay, M., et al., *alpha2,3-sialyltransferase ST3Gal III modulates pancreatic cancer cell motility and adhesion in vitro and enhances its metastatic potential in vivo.* PLoS One, 2010. **5**(9).
143. Murata, K., et al., *Expression of N-acetylglucosaminyltransferase V in colorectal cancer correlates with metastasis and poor prognosis.* Clin Cancer Res, 2000. **6**(5): p. 1772-7.

144. Guo, H.B., et al., *Specific posttranslational modification regulates early events in mammary carcinoma formation.* Proc Natl Acad Sci U S A, 2010. **107**(49): p. 21116-21.
145. Lee, J.H., et al., *N-Acetylglucosaminyltransferase V triggers overexpression of MT1-MMP and reinforces the invasive/metastatic potential of cancer cells.* Biochem Biophys Res Commun, 2013. **431**(4): p. 658-63.
146. Granovsky, M., et al., *Suppression of tumor growth and metastasis in Mgat5-deficient mice.* Nat Med, 2000. **6**(3): p. 306-12.
147. Seberger, P.J. and W.G. Chaney, *Control of metastasis by Asn-linked, beta1-6 branched oligosaccharides in mouse mammary cancer cells.* Glycobiology, 1999. **9**(3): p. 235-41.
148. Croci, D.O., et al., *Glycosylation-dependent lectin-receptor interactions preserve angiogenesis in anti-VEGF refractory tumors.* Cell, 2014. **156**(4): p. 744-58.
149. Dosaka-Akita, H., et al., *Expression of N-acetylglucosaminyltransferase v is associated with prognosis and histology in non-small cell lung cancers.* Clin Cancer Res, 2004. **10**(5): p. 1773-9.
150. Ito, Y., et al., *Elevated expression of UDP-N-acetylglucosamine: alphamannoside beta1,6 N-acetylglucosaminyltransferase is an early event in hepatocarcinogenesis.* Int J Cancer, 2001. **91**(5): p. 631-7.
151. Isaji, T., et al., *Functional roles of the bisecting GlcNAc in integrin-mediated cell adhesion.* Methods Enzymol, 2010. **480**: p. 445-59.
152. Sasai, K., et al., *The action of N-acetylglucosaminyltransferase-V is prevented by the bisecting GlcNAc residue at the catalytic step.* FEBS Lett, 2002. **522**(1-3): p. 151-5.
153. Yoshimura, M., et al., *Suppression of lung metastasis of B16 mouse melanoma by N-acetylglucosaminyltransferase III gene transfection.* Proc Natl Acad Sci U S A, 1995. **92**(19): p. 8754-8.
154. Pinho, S.S., et al., *E-cadherin and adherens-junctions stability in gastric carcinoma: functional implications of glycosyltransferases involving N-glycan branching biosynthesis, N-acetylglucosaminyltransferases III and V.* Biochim Biophys Acta, 2013. **1830**(3): p. 2690-700.
155. Zhao, Y., et al., *Branched N-glycans regulate the biological functions of integrins and cadherins.* FEBS J, 2008. **275**(9): p. 1939-48.
156. Isaji, T., et al., *Introduction of bisecting GlcNAc into integrin alpha5beta1 reduces ligand binding and down-regulates cell adhesion and cell migration.* J Biol Chem, 2004. **279**(19): p. 19747-54.
157. Zhao, Y., et al., *N-acetylglucosaminyltransferase III antagonizes the effect of N-acetylglucosaminyltransferase V on alpha3beta1 integrin-mediated cell migration.* J Biol Chem, 2006. **281**(43): p. 32122-30.
158. Thorpe, S.J., et al., *Blood group antigens in the normal and neoplastic bladder epithelium.* J Clin Pathol, 1983. **36**(8): p. 873-82.
159. Summers, J.L., et al., *Prognosis in carcinoma of the urinary bladder based upon tissue blood group abh and Thomsen-Friedenreich antigen status and karyotype of the initial tumor.* Cancer Res, 1983. **43**(2): p. 934-9.
160. Nagao, K., et al., *Evaluation of urinary CA19-9 levels in bladder cancer patients classified according to the combinations of Lewis and Secretor blood group genotypes.* Int J Urol, 2007. **14**(9): p. 795-9.
161. Kajiwara, H., et al., *Expression of carbohydrate antigens (SSEA-1, sialyl-Lewis X, DU-PAN-2 and CA19-9) and E-selectin in urothelial carcinoma of the renal pelvis, ureter, and urinary bladder.* Tokai J Exp Clin Med, 2005. **30**(3): p. 177-82.
162. Ishimura, H., et al., *N-acetylglucosaminyltransferase V and beta1-6 branching N-linked oligosaccharides are associated with good prognosis of patients with bladder cancer.* Clin Cancer Res, 2006. **12**(8): p. 2506-11.

163. Langkilde, N.C., et al., *Nuclear volume and expression of T-antigen, sialosyl-Tn-antigen, and Tn-antigen in carcinoma of the human bladder. Relation to tumor recurrence and progression.* Cancer, 1992. **69**(1): p. 219-27.
164. Videira, P.A., et al., *ST3Gal.I sialyltransferase relevance in bladder cancer tissues and cell lines.* BMC Cancer, 2009. **9**: p. 357.
165. Carrascal, M.A., et al., *Sialyl Tn-expressing bladder cancer cells induce a tolerogenic phenotype in innate and adaptive immune cells.* Mol Oncol, 2014. **8**(3): p. 753-65.
166. Schultz, M.J., et al., *ST6Gal-I sialyltransferase confers cisplatin resistance in ovarian tumor cells.* J Ovarian Res, 2013. **6**(1): p. 25.
167. Swindall, A.F. and S.L. Bellis, *Sialylation of the Fas death receptor by ST6Gal-I provides protection against Fas-mediated apoptosis in colon carcinoma cells.* J Biol Chem, 2011. **286**(26): p. 22982-90.
168. Liu, Z., et al., *ST6Gal-I regulates macrophage apoptosis via α2-6 sialylation of the TNFR1 death receptor.* J Biol Chem, 2011. **286**(45): p. 39654-62.
169. Mazurek, N., et al., *Cell-surface galectin-3 confers resistance to TRAIL by impeding trafficking of death receptors in metastatic colon adenocarcinoma cells.* Cell Death Differ, 2012. **19**(3): p. 523-33.
170. Swindall, A.F., et al., *ST6Gal-I protein expression is upregulated in human epithelial tumors and correlates with stem cell markers in normal tissues and colon cancer cell lines.* Cancer Res, 2013. **73**(7): p. 2368-78.
171. Kudo, T., et al., *N-glycan alterations are associated with drug resistance in human hepatocellular carcinoma.* Mol Cancer, 2007. **6**: p. 32.
172. Ma, H., et al., *Functional roles of glycogene and N-glycan in multidrug resistance of human breast cancer cells.* IUBMB Life, 2013. **65**(5): p. 409-22.
173. Zhang, Z., et al., *Glycomic alterations are associated with multidrug resistance in human leukemia.* Int J Biochem Cell Biol, 2012. **44**(8): p. 1244-53.
174. Liang, X.J., et al., *Mislocalization of membrane proteins associated with multidrug resistance in cisplatin-resistant cancer cell lines.* Cancer Res, 2003. **63**(18): p. 5909-16.
175. Beretta, G.L., et al., *Increased levels and defective glycosylation of MRPs in ovarian carcinoma cells resistant to oxaliplatin.* Biochem Pharmacol, 2010. **79**(8): p. 1108-17.
176. Paterson, J.K., et al., *Human ABCB6 localizes to both the outer mitochondrial membrane and the plasma membrane.* Biochemistry, 2007. **46**(33): p. 9443-52.
177. Pasin, E., et al., *Superficial bladder cancer: an update on etiology, molecular development, classification, and natural history.* Rev Urol, 2008. **10**(1): p. 31-43.
178. Julien, S., et al., *ST6GalNAc I expression in MDA-MB-231 breast cancer cells greatly modifies their O-glycosylation pattern and enhances their tumourigenicity.* Glycobiology, 2006. **16**(1): p. 54-64.
179. Flucke, U., et al., *Expression of mucin-associated carbohydrate core antigens in esophageal squamous cell carcinomas.* Anticancer Res, 2001. **21**(3C): p. 2189-93.
180. Victorzon, M., et al., *Sialyl Tn antigen is an independent predictor of outcome in patients with gastric cancer.* Int J Cancer, 1996. **65**(3): p. 295-300.
181. Lin, J.C., et al., *Molecular events associated with epithelial to mesenchymal transition of nasopharyngeal carcinoma cells in the absence of Epstein-Barr virus genome.* J Biomed Sci, 2009. **16**: p. 105.
182. Damrauer, J.S., et al., *Intrinsic subtypes of high-grade bladder cancer reflect the hallmarks of breast cancer biology.* Proc Natl Acad Sci U S A, 2014. **111**(8): p. 3110-5.
183. Pinto-Leite, R., et al., *Genomic characterization of three urinary bladder cancer cell lines: understanding genomic types of urinary bladder cancer.* Tumour Biol, 2014. **35**(5): p. 4599-617.

184. Bindea, G., J. Galon, and B. Mlecnik, *CluePedia Cytoscape plugin: pathway insights using integrated experimental and in silico data.* Bioinformatics, 2013. **29**(5): p. 661-3.
185. Bindea, G., et al., *ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks.* Bioinformatics, 2009. **25**(8): p. 1091-3.
186. Sjödahl, G., et al., *A molecular taxonomy for urothelial carcinoma.* Clin Cancer Res, 2012. **18**(12): p. 3377-86.
187. Volkmer, J.P., et al., *Three differentiation states risk-stratify bladder cancer into distinct subtypes.* Proc Natl Acad Sci U S A, 2012. **109**(6): p. 2078-83.
188. Choi, W., et al., *Identification of distinct basal and luminal subtypes of muscle-invasive bladder cancer with different sensitivities to frontline chemotherapy.* Cancer Cell, 2014. **25**(2): p. 152-65.
189. Steentoft, C., et al., *Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology.* EMBO J, 2013. **32**(10): p. 1478-88.
190. Ferreira, R., et al., *Lifelong exercise training modulates cardiac mitochondrial phosphoproteome in rats.* J Proteome Res, 2014. **13**(4): p. 2045-55.
191. Mi, H., et al., *The PANTHER database of protein families, subfamilies, functions and pathways.* Nucleic Acids Res, 2005. **33**(Database issue): p. D284-8.
192. Kuhn, M., et al., *STITCH: interaction networks of chemicals and proteins.* Nucleic Acids Res, 2008. **36**(Database issue): p. D684-8.
193. Drayton, R.M. and J.W. Catto, *Molecular mechanisms of cisplatin resistance in bladder cancer.* Expert Rev Anticancer Ther, 2012. **12**(2): p. 271-81.
194. Tatokoro, M., et al., *Potential role of Hsp90 inhibitors in overcoming cisplatin resistance of bladder cancer-initiating cells.* Int J Cancer, 2012. **131**(4): p. 987-96.
195. Felder, M., et al., *MUC16 (CA125): tumor biomarker to cancer therapy, a work in progress.* Mol Cancer, 2014. **13**: p. 129.
196. Yoon, C., et al., *CD44 expression denotes a subpopulation of gastric cancer cells in which Hedgehog signaling promotes chemotherapy resistance.* Clin Cancer Res, 2014. **20**(15): p. 3974-88.
197. Wang, S.J. and L.Y. Bourguignon, *Role of hyaluronan-mediated CD44 signaling in head and neck squamous cell carcinoma progression and chemoresistance.* Am J Pathol, 2011. **178**(3): p. 956-63.
198. Karsten, U. and S. Goletz, *What makes cancer stem cell markers different?* Springerplus, 2013. **2**(1): p. 301.
199. Campos, D., et al., *Probing the O-glycoproteome of gastric cancer cell lines for biomarker discovery.* Mol Cell Proteomics, 2015. **14**(6): p. 1616-29.
200. Manvar, A.M., et al., *Prognostic value of CA 125 in transitional cell carcinoma of the bladder.* Expert Rev Anticancer Ther, 2010. **10**(12): p. 1877-81.

Appendix

Appendix A. Research article “Abnormal Protein Glycosylation and Activated PI3K/Akt/mTOR Pathway: Role in Bladder Cancer Prognosis and Targeted Therapeutics.”

Appendix B. Proteins identified with high confidence level in Tn-negative, blood group A negative, STn-positive basal-like chemoresistant tumors recovered from formalin-fixed paraffin embedded tissues.

Appendix C. Identified membrane glycoproteins from Tn-negative, blood group A negative, STn-positive basal-like chemoresistant tumors, with O-GalNAc as posttranslational modifications after neuraminiase treatment.

Appendix A

PLOS ONE

RESEARCH ARTICLE

Abnormal Protein Glycosylation and Activated PI3K/Akt/mTOR Pathway: Role in Bladder Cancer Prognosis and Targeted Therapeutics

Céu Costa[1,2,3☯], Sofia Pereira[1,2,3☯], Luís Lima[1,4,5], Andreia Peixoto[1], Elisabete Fernandes[1], Diogo Neves[1], Manuel Neves[1], Cristiana Gaiteiro[1], Ana Tavares[1,6], Rui M. Gil da Costa[1,7], Ricardo Cruz[8], Teresina Amaro[9], Paula A. Oliveira[10], José Alexandre Ferreira[1,11]*, Lúcio L. Santos[1,3,12]*

1 Experimental Pathology and Therapeutics Group, Portuguese Institute of Oncology, Rua Dr. António Bernardino de Almeida, Porto, Portugal, **2** ICBAS, Abel Salazar Biomedical Sciences Institute, University of Porto, Porto, Portugal, **3** Health Sciences Faculty of University Fernando Pessoa, Porto, Portugal, **4** Nucleo de Investigação e Informação em Farmácia - Centro de Investigação em Saúde e Ambiente (CISA), School of Allied Health Sciences – Polytechnic Institute of Oporto, Porto, Portugal, **5** Institute of Pathology and Molecular Immunology of the University of Porto (IPATIMUP), Porto, Portugal, **6** Department of Pathology, Portuguese Institute of Oncology, Porto, Portugal, **7** Faculty of Engineering, Laboratory for Process, Environment, Biotechnology and Energy Engineering (LEPABE), University of Porto, Porto, Portugal, **8** Department of Urology, Portuguese Institute of Oncology, Porto, Portugal, **9** Department of Urology, Hospital Pedro Hispano, Matosinhos, Portugal, **10** Department of Veterinary Sciences, CITAB, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal, **11** Mass Spectrometry Center of the University of Aveiro, Campus de Santiago, Aveiro, Portugal, **12** Department of Surgical Oncology, Portuguese Institute of Oncology, Porto, Portugal

☯ These authors contributed equally to this work.
* josealexandreferreira@ua.pt (JAF); llarasantos@gmail.com (LLS)

Citation: Costa C, Pereira S, Lima L, Peixoto A, Fernandes E, Neves D, et al. (2015) Abnormal Protein Glycosylation and Activated PI3K/Akt/mTOR Pathway: Role in Bladder Cancer Prognosis and Targeted Therapeutics. PLoS ONE 10(11): e0141253. doi:10.1371/journal.pone.0141253

Editor: Francisco X. Real, Centro Nacional de Investigaciones Oncológicas (CNIO), SPAIN

Received: July 28, 2015

Accepted: October 6, 2015

Published: November 16, 2015

Data Availability Statement: All relevant data are within the paper.

Funding: This work was supported by Portuguese Foundation for Science and Technology (FCT) Postdoctoral grants SFRH/BPD/66288/2009 (José Alexandre Ferreira), SFRH/BPD/101827/2014 (Luis Lima), SFRH/BPD/85462/2012 (Rui Gil da Costa) and PhD grants SFRH/BD/103571/2014 (Elisabete Fernandes) and SFRH/BD/111242/2015 (Andreia Peixoto). FCT is co-financed by European Social Fund (ESF) under Human Potential Operation Programme (POPH) from National Strategic

Abstract

Muscle invasive bladder cancer (MIBC, stage ≥T2) is generally associated with poor prognosis, constituting the second most common cause of death among genitourinary tumours. Due to high molecular heterogeneity significant variations in the natural history and disease outcome have been observed. This has also delayed the introduction of personalized therapeutics, making advanced stage bladder cancer almost an orphan disease in terms of treatment. Altered protein glycosylation translated by the expression of the sialyl-Tn antigen (STn) and its precursor Tn as well as the activation of the PI3K/Akt/mTOR pathway are cancer-associated events that may hold potential for patient stratification and guided therapy. Therefore, a retrospective design, 96 bladder tumours of different stages (Ta, T1-T4) was screened for STn and phosphorylated forms of Akt (pAkt), mTOR (pmTOR), S6 (pS6) and PTEN, related with the activation of the PI3K/Akt/mTOR pathway. In our series the expression of Tn was residual and was not linked to stage or outcome, while STn was statically higher in MIBC when compared to non-muscle invasive tumours ($p = 0.001$) and associated decreased cancer-specific survival (log rank $p = 0.024$). Conversely, PI3K/Akt/mTOR pathway intermediates showed an equal distribution between non-muscle invasive bladder cancer (NMIBC) and MIBC and did not associate with cancer-specif survival (CSS) in any of

PLOS ONE | Glycosylation and PI3K/Akt/mTOR Pathway in Bladder Cancer

Reference Framework (NSRF). The authors also acknowledge financial support from ICBAS-UP (Céu Costa and Sofia Pereira) and the Portuguese Association of Urology/Pfizer prize 2013. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

these groups. However, the overexpression of pAKT, pmTOR and/or pS6 allowed discriminating STn-positive advanced stage bladder tumours facing worst CSS (p = 0.027). Furthermore, multivariate Cox regression analysis revealed that overexpression of PI3K/Akt/mTOR pathway proteins in STn+ MIBC was independently associated with approximately 6-fold risk of death by cancer (p = 0.039). Mice bearing advanced stage chemically-induced bladder tumours mimicking the histological and molecular nature of human tumours were then administrated with mTOR-pathway inhibitor sirolimus (rapamycin). This decreased the number of invasive lesions and, concomitantly, the expression of STn and also pS6, the downstream effector of the PI3K/Akt/mTOR pathway. In conclusion, STn was found to be marker of poor prognosis in bladder cancer and, in combination with PI3K/Akt/mTOR pathway evaluation, holds potential to improve the stratification of stage disease. Animal experiments suggest that mTOR pathway inhibition could be a potential therapeutic approach for this specific subtype of MIBC.

Introduction

Bladder cancer is the second most deadly genitourinary tumour and presents significantly worse prognosis upon *muscularis propria* invasion [1]. Approximately 20–30% of the newly diagnosed cases are muscle invasive bladder cancers (MIBC; T2-T4 stages), while 50% are non-muscle invasive bladder tumours (NMIBC) with high potential to progress to invasion. MIBC treatment includes cystectomy and (neo)adjuvant cisplatin-based chemotherapy regimens [2]. However, significant variations in the natural history of the disease and responses to treatment can be observed between tumours with identical histological features, reflecting their high molecular heterogeneity [3]. Furthermore, approximately 50% of cases develop metastasis within 5 years, urging the identification of biomarkers to assist prognostication and the development of more effective targeted therapeutics [4].

To meet this need, we have recently addressed the expression of the cancer-associated sialyl-Tn antigen (STn) on a small prospective series of unselected bladder cancer patients [5]. STn is an abnormal post-translational modification that results from a premature stop in cell-membrane proteins *O*-glycosylation by sialylation of the Tn antigen (Fig 1A). In bladder tumours, STn it was mainly present in advanced stage cases, while absent from most low-grade NMIBC [5]. Moreover, it was not expressed by the normal urothelium, denoting a cancer-specific nature [5]. Studies *in vitro* showed that STn expression endowed bladder cancer cells with high invasion capability [5] and an immunotolerogenic phenotype, potentially favoring disease dissemination [6]. Alterations in cell-surface protein glycosylation have be implicated in the activation of intracellular oncogenic signalling pathways [7], including the phosphoinositide-3 kinase (PI3K)/Akt signalling pathway [8] which is thought to play a critical role in bladder cancer development. These preliminary observations support the hypothesis that STn expression may play a key role in disease outcome, which warrants a deeper investigation. Several studies also suggest that Tn antigen, which is a precursor of STn, may be also implicated in oncogenic events [7]; however nothing is known about the expression of this glycan in bladder tumours.

The phosphatidylinositol-3-kinase (PI3K)/Akt and the mammalian target of rapamycin (mTOR) pathways are interconnected signaling cascades essential for bladder cell growth and survival (Fig 1B). The PI3K/Akt/mTOR or mTOR pathway integrates a multiplicity of extracellular signals to regulate downstream signaling and protein synthesis, which ultimately leads to

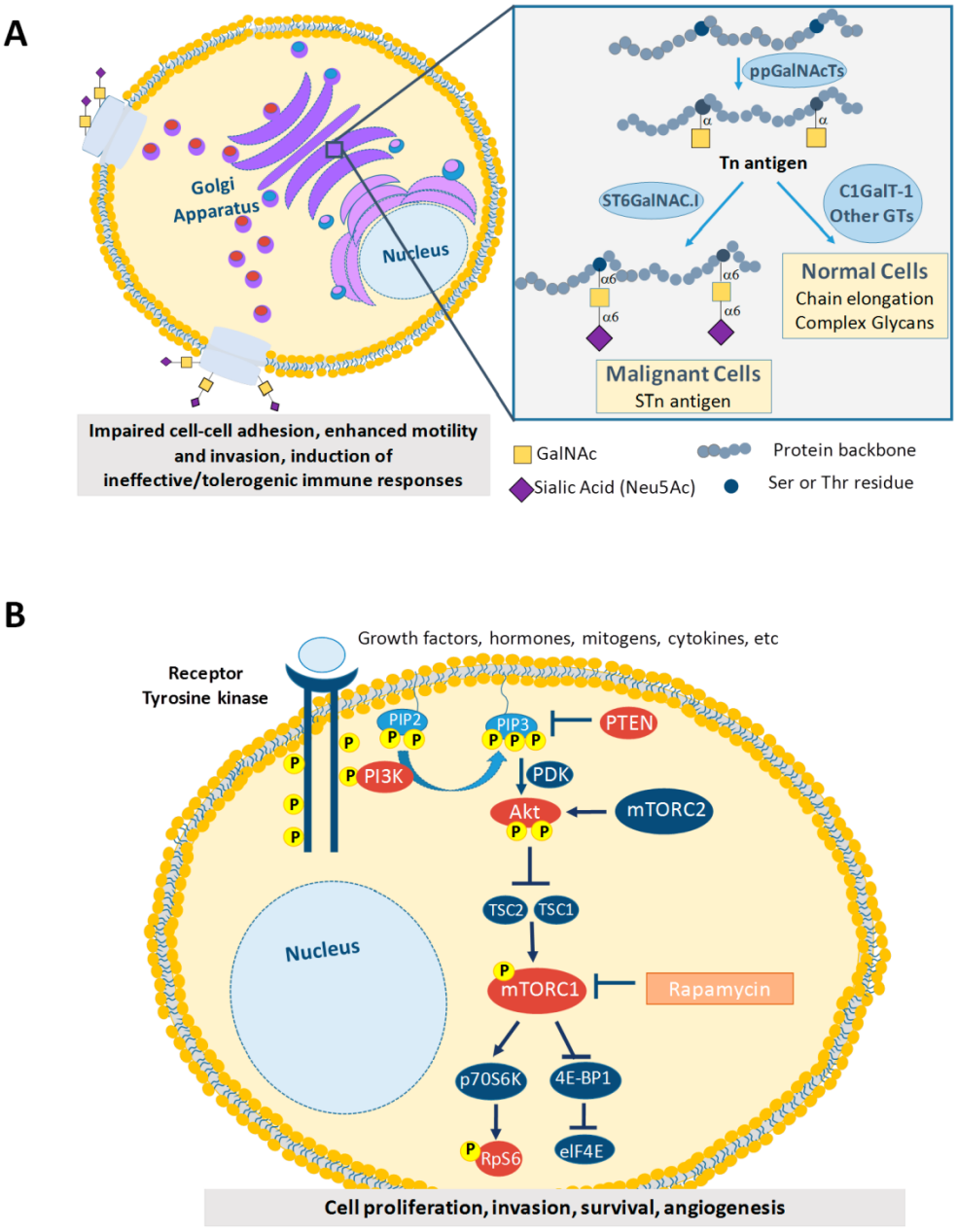


Fig 1. Schematic representation of membrane protein *O*-glycosylation and the PI3K/Akt/mTOR pathways. A) Representation of membrane protein *O*-glycosylation with emphasis on the STn expression by cancer cells. This is a highly regulated process of critical importance for protein stability and function. Briefly, newly synthesized proteins are *O*-glycosylated in the Golgi apparatus by the ppGalNAcTs-mediated addition of GalNAc moiety to Ser/Thr residues. This originates the Tn antigen (GalNAc-O-Ser/Thr-protein backbone), which is the simplest O-glycan. In normal cells these chains are extended through the sequential addition of other sugars first by CGALT-1 and then other enzymes. This culminates in highly complex, heterogeneous and elongated glycans often terminated by ABO or Lewis blood group related antigens (left drawing). In cancer cells the Tn antigen is immediately sialylated by ST6GalNAc.I, originating the STn antigen (Neu5Ac-GalNAc-O-Ser/Thr-protein backbone), thereby inhibiting further chain elongation (right drawing). The expression of STn at the cell surface influences cell-cell adhesion and cancer cell recognition, favouring motility, invasion and immune escape. B) Schematic representation of the PI3K/Akt/mTOR pathway, which is ubiquitously activated in bladder tumours. This is a highly conserved pathway regulated mainly by a wide variety of extracellular signals, including mitogenic growth factors, hormones, nutrients, cellular energy levels, and stress conditions. These signals activate tyrosine receptor kinases that recruit PI3K, which catalyses the conversion of membrane-bound PIP2 to PIP3. Then Akt and PDK-1 are activated through binding to PIP3. PTEN preferentially dephosphorylates PIP3, inhibiting signalling progression. Full Akt activation requires double phosphorylation by PDK-1 itself and PDK-2 (not shown). Akt phosphorylates mTOR directly or may also inactivate TSC1/TSC2 complex, inhibiting mTOR inactivation. mTORC1 triggers cell growth and proliferation by phosphorylating eukaryotic translation regulators, among these p70S6 kinase (p70S6K or S6K1) that, in turn, phosphorylates the

ribosomal protein S6 (pS6), and the eukaryotic translation initiation factor 4E–binding protein 1 (4E-BP1). For the protein mTOR to activate its signalling cascade, it must form the rapamycin-sensitive ternary complex mTORC1. Key PI3K/Akt/mTOR-pathway proteins pAkt, pmTOR and pS6 explored in this studied are highlighted by orange circles.

doi:10.1371/journal.pone.0141253.g001

a competitive growth advantage, metastatic competence, angiogenesis, and therapy resistance [9]. The signaling cascade begins with PI3K activation in the cell membrane followed by serine/threonine kinase Akt cell membrane translocation and activation. The best studied downstream substrate of Akt is the serine/threonine kinase mTOR, whose downstream effector is S6 kinase-1 (S6K1). In particular, a subset of mTOR pathway alterations have been shown to occur in bladder cancer, such as mutations in *PIK3CA* gene, which culminates with increased mTOR signaling and bladder cancer cells resistance to apoptosis [10]. Moreover, the pharmacological or biochemical inhibition of the PI3K pathway drastically reduced the invasive capacity of bladder cancer cell lines. Furthermore, over half of primary human bladder tumours present high Akt phosphorylation and the aberrant activation of this pathway has been suggested to contribute to invasion [11]. Another event influencing mTOR pathway activation in bladder tumours involves the loss of tumor suppressor PTEN (phosphatase and tensin homolog deleted on chromosome ten) function [12]. PTEN normally suppresses activation of the PI3K/Akt/mTOR pathway antagonizing PI3K and preventing activation of Akt and PDK-1. PTEN also functions to regulate chemotaxis and cell motility, thereby promoting tumor invasion [13]. In summary, there are evidences that a comprehensive evaluation of PI3K/Akt/mTOR pathway associated proteins may hold significant potential for value for patient stratification. Moreover, many preclinical and clinical studies support that mTOR inhibitors, such as sirolimus (rapamycin) and their derivatives may improve cancer treatment [13,14].

Based on these observations we hypothesize that Tn and/or STn may act synergistically with the mTOR pathway to drive bladder cancer progression. As such, we have devoted to evaluating the expression of STn and proteins associated with the activation of the PI3K/Akt/mTOR pathway activation in bladder tumours at different stages. We anticipate that the combination of extracellular and intracellular oncogenic events may improve patient stratification and provide insights for novel therapeutics. Furthermore we have estimated the impact of sirolimus in chemically-induced urothelial tumours in mice, envisaging the creation of a rationale for more effective bladder cancer therapeutics.

Materials and Methods

Ethics Statement

This work involves experiences in tumour samples of patients diagnosed with bladder cancer in the Portuguese Insitute of Oncology of Porto. All procedures were performed after patient's written informed consent and approved by the Ethics Committee of Portuguese Institute of Oncology—Porto. All clinicopathological information was obtained from patients' clinical records.

It also involves animal experiments. All procedures involving animals were performed in accordance with the European Directive 2010/63/EU. During the course of this study, the animals were fed *ad libitum* with standardized food (Tecklad Global Diet, Harlan, Spain). The following protocol was approved by the Portuguese Ethics Committee for Animal Experimentation (Direção Geral de Veterinária, Approval no. 520/000/000/2003). All mice used in the experiment were acclimatized for one week under routine laboratory conditions before starting the experiments. They were housed randomly in groups of 4–5 in plastic cages, with hard wood chips for bedding. The animals were maintained in a room with a controlled

temperature of 23±2°C, a 12-hour light/dark cycle and 55±5% humidity. The animals' drinking solutions were changed once a week or earlier if necessary, and the volume drunk was recorded. Weekly food intake was also noted. All mice were monitored throughout the experiment for signs of distress and loss of body weight. The animals were sacrificed with 0.4% sodium pentobarbital (1 ml/Kg, intraperitoneal).

Population

This study was performed in a retrospective series of 96 formalin-fixed paraffin-embedded bladder tumours obtained from archived paraffin blocks at the Portuguese Institute of Oncology—Porto (IPOP), Portugal. Bladder tumours were extracted from 82 men and 14 women, ranging in age from 38 to 92 years (median of 69.5 years), admitted and treated at the IPOP between 2005 and 2007. Forty seven of the examined tumours were histologically classified as NMBIC (Ta and T1) and 49 as invasive lesions (T2-T4). Sixteen were low grade and 80 were high grade tumours, according to the 2004 WHO grading criteria. Furthermore, carcinoma *in situ* (CIS) was found concomitantly in 20.8% of the patients. The average follow up time period was 45 months (1–134 months). Cystectomy was performed in 64 patients (66.7%) while the other 32 (33.3%) were submitted to transurethral resection. Lymphadenectomy was performed in approximately 47% of the patients and from those 37% presented metastasis. Fifty four (56.3%) tumours were primary and 42 (43.7%) were recurrent tumors. From the recurrent tumours, 38% had no prior treatment, 27% were treated with Mitomicin C, 11% with BCG and 19% were submitted to both treatments. Moreover 5% of these patients were treated with neoadjuvant chemotherapy prior to the cystectomy. Table 1 summarizes the clinicopathological information.

Cancer-specific survival (CSS) was defined as the period between the tumour removal by surgery and either patient death by cancer or the last follow-up information. All procedures were performed after patient's informed consent and approved by the Ethics Committee of IPO-Porto. All clinicopathological information was obtained from patients' clinical records.

Immunohistochemistry

The expressions of STn antigen, its precursor Tn, and phosphorylated forms of Akt (pAkt), mTOR (pmTOR), S6 (pS6) and PTEN in bladder tumours were accessed by immunohistochemistry using the avidin/streptavidin peroxidase method, as described by Ferreira et al. [5]. Information on the primary antibodies and dilutions used in this study are summarized in Table 2. Immunoreactivity was revealed using diaminobenzidine (DAB, Thermo Scientific LabVision) as chromogen and sections were counterstained with Harris's hematoxylin. Negative controls were performed by replacing the primary antibody with 5% bovine serum albumin (BSA). Positive controls were known positive tissues for the antigens under study.

Immunohistochemistry scoring of human tumours

The immunostained sections were assessed double-blindly by light microscopy by two independent observers (CC and SP) and validated by an experienced pathologist (TA). Disaccording readings were re-analyzed using a double-headed microscope (Olympus BX46; Olympus Corporation), and consensus was reached. A semi-quantitative approach was established to score the immunohistochemical labeling based on the extent and intensity of the staining.

Given the absence of Tn and STn in the healthy urothelium [5], tumours were classified as positive for these antigens when membrane and/or cytoplasmic immunoreactivity were observed in more than 5% of the tumour, as described by Ferreira et al. [5,15]. pAkt, pmTOR, pS6 and PTEN expressions were scored according to the staining intensity (weak-1 point;

Table 1. Clinical-pathological data of the studied sample (*n* = 96).

Age, *years*		
	median [min—max]	69.5 [38–92]
Gender, *n* (%)		
	Male	82 (85.4%)
	Female	14 (14.6%)
Stage, *n* (%)		
	Ta	27 (28.1%)
	T1	20 (20.8%)
	T2	9 (9.4%)
	T3	20 (20.8%)
	T4	20 (20.8%)
Grade, n (%)		
	Low	16 (16.7%)
	High	80 (83.3%)
Recurrence status, n(%)		
	Primary	54 (56.3%)
	Recurrent	42 (43.7%)
Associated Cis, n(%)		
	No	76 (79.2%)
	Yes	20 (20.8%)
Metastasis, n(%)		
	No	19 (63.3%)
	Yes	11 (36.7%)
Follow-up, *n (%)*		
	Alive, lost or death from other causes	67 (69.8%)
	Death from cancer	29 (30.2%)

doi:10.1371/journal.pone.0141253.t001

moderate-2 points; strong-3 points) multiplied by the percentage of positive cells (0–5%-0 points; >5–25%-1 point; >25–50%-2 points; >50–75%-3 points; >75–100%-4 points). Based on the classification proposed by Nishikawa et al. [16], tumours with a score <6 were considered negative, whereas those with a score≥6 were classified as positive (overexpression). pAkt was evaluated based on nuclear immunoreactivity, pmTOR and pS6 based on cytoplasmic expression and PTEN on both cytoplasmic and nuclear staining, as suggested by other publications [17,18].

Animal experiments with sirolimus and immunohistochemistry scoring

Histological sections of Imprinting Control Region (ICR) mice bearing N-butyl-N-(4-hydroxybutyl) nitrosamine (BBN)-induced bladder lesions, resulting from our previous work on the impact of sirolimus on bladder cancer [19], were elected for this study. Briefly, four-week-old male ICR mice (25g; Harlan, Barcelona, Spain) were randomly distributed into four groups, as described in detail in a previous publication [18]. Group 1 (n = 6) included mice exposed to 0.05% BBN for 12 weeks followed by tap water for 8 weeks (total of 20 weeks). Group 2 (n = 7) included mice treated with 0.05% BBN solution for twelve weeks, maintained with normal tap water for another week, administrated intraperitoneally with mTOR-inhibitor sirolimus (1.5 mg/kg; Wyeth) for five days a week for six consecutively weeks, i.e. until the 19th week, followed by another week of tap water (total of 20 weeks). Group 3 (n = 6) included mice exposed to 0.05% BBN for 12 weeks followed by tap water for 11 weeks (total of 23 weeks). Group 4

Table 2. Antibodies used in the immunohistochemical analysis.

Antibody	Vendor	Clone	Dilution
Tn	Non-commercial Hybridoma*	IE3	1:5
STn	Non-commercial Hybridoma*	TKH2	1:20
Ki-67	Dako	MIB-1	1:100
p53	Dako	DO-7	1:100
Phos-AKT	Cell Signaling	Ser473 (736E11)	1:50
Phos-mTOR	Cell Signaling	Ser2448(49F9)	1:100
Phos-S6	Cell Signaling	Ser240/244 polyclonal	1:75
PTEN	Cell Signaling	D4.3 XP	1:50

*Kindly provided by Prof. Celso Reis (IPATIMUP, UP, Portugal)

doi:10.1371/journal.pone.0141253.t002

(n = 7) included mice treated with 0.05% BBN and sirolimus, as described for Group 2, but with an exposure to tap water afterwards of 3 weeks (total of 23 weeks). Group 3 and 4 were created to estimate the possibility of late relapse and/or molecular alterations resulting from prolonged survival. All procedures were performed in accordance with the European Directive 2010/63/EU. During the course of this study, the animals were fed *ad libitum* with standardized food (Tecklad Global Diet, Harlan, Spain). The histological changes induced by these experiments included both preneoplastic and neoplastic lesions with invasive potential and invasive tumours, as described in detail by Oliveira et al. [18]. Herein, lesions of high invasive potential and muscle invasive tumours were screened for STn and pS6 by immunohistochemistry, as described in detail for human tumours, since the antibodies used are reactive against both human and mice. Both the intensity and the extension of immunostaining were taken into consideration to score the expression of the antigens, as described in the previous section. The bladder lesions and immunostaining were assessed double-blindly by two independent observers (CC and SP) and validated by an experienced veterinary pathologist (RMGC).

Statistical analysis

Statistical data analysis was performed with IBM Statistical Package for Social Sciences—SPSS for Windows (version 20.0). Chi-square analysis was used to compare categorical variables. Kaplan-Meier survival curves were used to evaluate correlation between STn expression and cancer-specific survival (CSS) and were compared using log-rank test. Furthermore, multivariate Cox regression analysis was performed to assess the individual effect of the evaluated markers on patient's survival and adjust to potential confounders (variables that could affect CSS of NMIBC and MIBC patients). The correlation between PI3K/Akt/mTOR pathway molecules was performed using Spearman rho test.

Results

Altered protein glycosylation, translated by the expression of the STn antigen and its precursor Tn, PI3K/Akt/mTOR pathway molecules (pAkt, pmTOR, pS6), and PTEN inactivation, are salient features of bladder tumours. Herein we have devoted to a comprehensive analysis of these molecular alterations in a series of bladder cancer patients at different stages of the disease, envisaging biomarkers of poor cancer-specific survival.

Our dataset was composed by 47 NMIBC and 49 MIBC patients, as showed in Table 1. According to Fig 2, NMIBC presented a higher cancer-specific survival (CSS; mean CSS: 119 months) than MIBC patients (mean CSS: 43 months; log rank, $p<0.001$). These results

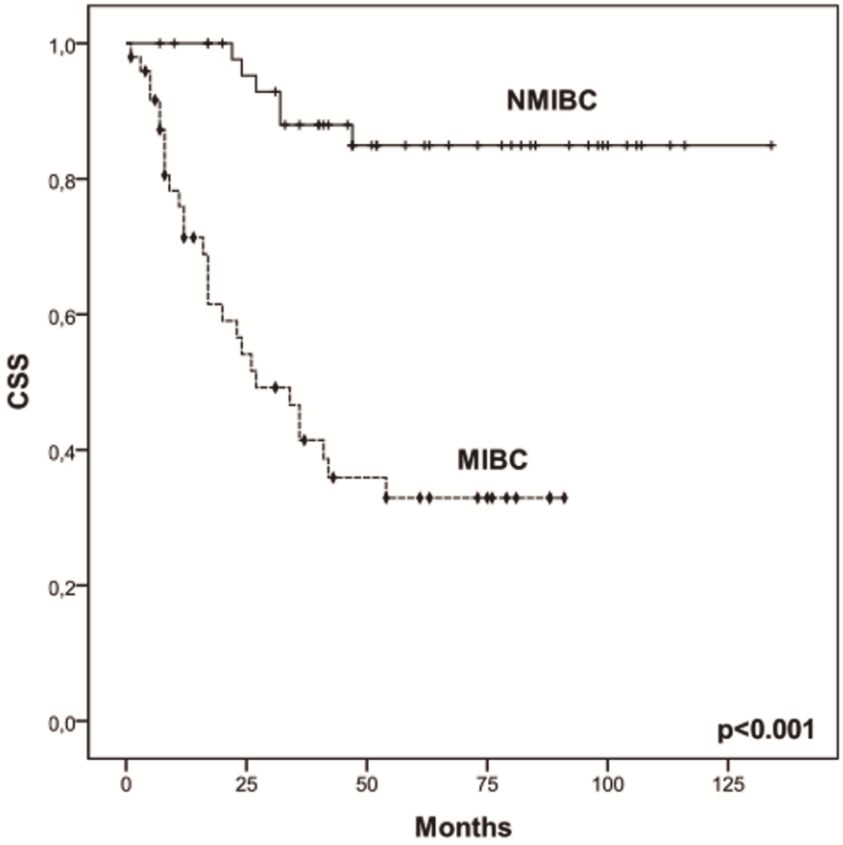


Fig 2. Association between disease groups and cancer-specific survival (CSS) in the studied patients. Kaplan-Meier analysis showing the CSS of NMIBC (Ta and T1) and s of MIBC (T2,T3 and T4). Comparison performed by log-rank test (p<0.001); + censored NMIBC patients; ♦ censored MIBC patients.

doi:10.1371/journal.pone.0141253.g002

demonstrated that our series reflected the natural course of disease and highlighted the significantly lower CSS of MIBC compared to NMIBC cases. Therefore, particular interest was set in the identification of biomarkers for late stage disease based on the comparison between NMIBC and MIBC.

Tn and STn antigen expressions in bladder cancer

The Tn antigen was observed in approximately 10% of NMBC and MIBC (Table 2) and its expression was residual, did not exceeding 5% of the tumour area and without any defined pattern. On the other hand, the STn antigen was detected in approximately 60% of the studied bladder tumours, which is in accordance with our previous findings [5]. The antigen was predominately expressed at the cell membrane, although cytoplasmic staining could also be observed. The STn antigen presented a focal expression that did not exceed 30% of the tumour area for the majority of the positive cases, irrespectively of their histological origin. STn was mainly expressed by dedifferentiated cells in tumours showing *lamina propria* (T1; 60%) and *muscularis propria* (≥ T2; approximately 60–90%) invasion; conversely the percentage of positive Ta was lower than 30% ($p<0.001$; Fig 3A). Although without statistical significance, in Ta tumours STn positive cells were mainly present in superficial tumour layers away from the vessels. Conversely, STn positive cells in T1 tumours (Fig 3B) were observed accompanying and/

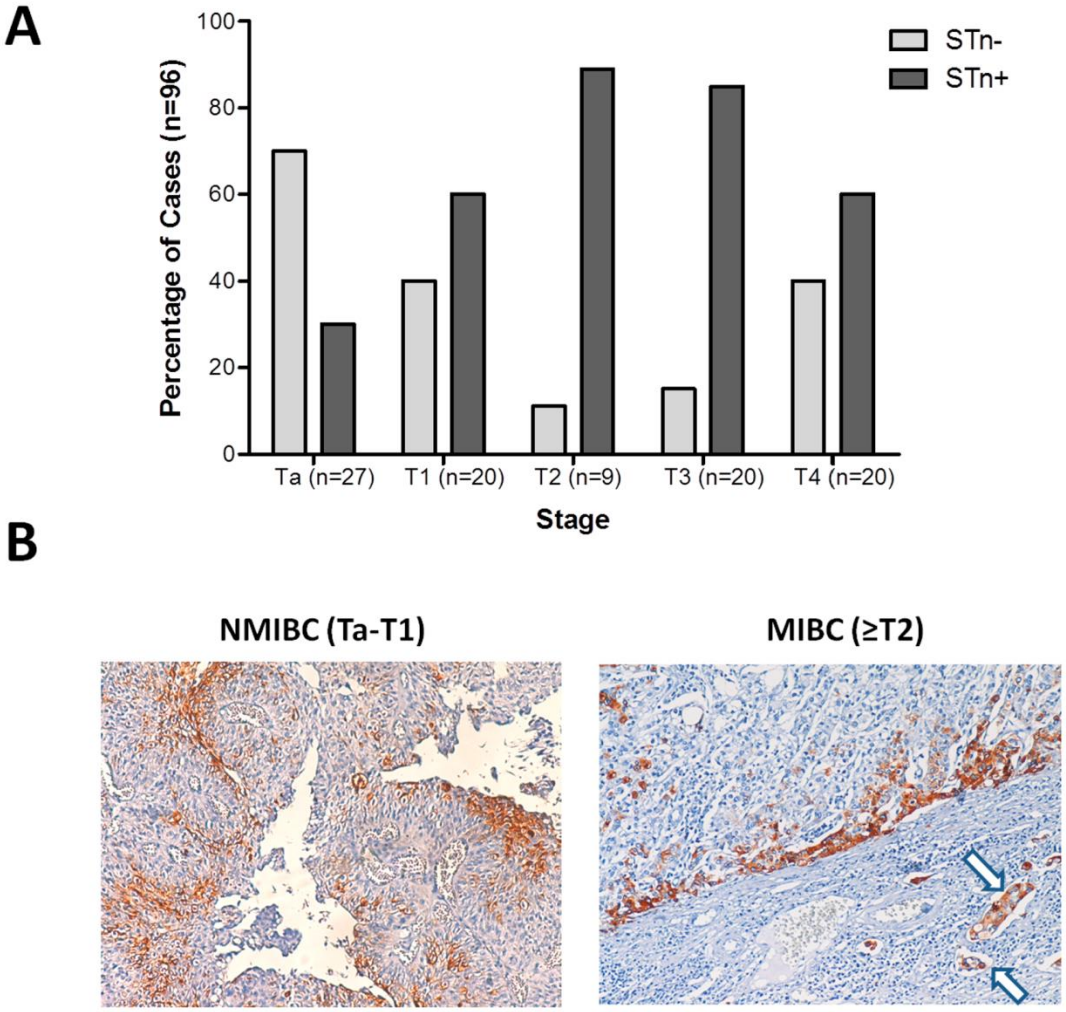


Fig 3. STn expression in different bladder tumors stages. (A) Distribution of STn negative and positive tumors along the different stages of bladder cancer; (B) Representative images of STn staining in NMIBC and MIBC. Left—NMIBC showing a predominance of STn positive cells in the superficial layers, away from the fibrovascular support; note vessels without positive cells. Right—MIBC showing the invasion front with STn positively stained cells; note positive STn urothelial cells in the vessels (arrow), suggesting possible involvement in metastasis.

doi:10.1371/journal.pone.0141253.g003

or invading the basal layer (Fig 3B), while in MIBC these cells were mostly found in the invasion fronts (Fig 3B) and invading and/or inside the vessels, which suggests a role in invasion and disease dissemination. Reinforcing these observations, the presence of STn antigen was statistically higher in MIBC when compared to NMIBC ($p = 0.001$, Table 3).

PI3K/Akt/mTOR pathway in bladder cancer

The evaluation of the PI3K/Akt/mTOR/S6 pathway was done using antibodies for active phosphorylated forms of Akt (pAkt), mTOR (pmTOR), and S6 (pS6). PTEN, that negatively regulates Akt signalling, was also evaluated.

pAkt was detected both in the cytoplasm and nucleus. In NMIBC cases several areas with different intensity of expression were observed (Fig 4A), denoting a heterogeneous pattern that was not evident in MIBC (Fig 4B). Furthermore, stromal cells of MIBC positive cases showed enhanced staining intensity mainly in the areas close to the tumour. pmTOR immunoreactivity

Table 3. Association between the evaluated markers and the stage of disease.

	Bladder Cancer		
	NMIBC n (%)	MIBC n (%)	P
Tn			
Negative	41 (87.2)	45 (91.8)	
Positive	6 (12.8)	4 (8.2)	0.461
STn			
Negative	27 (57.4)	12 (24.5)	
Positive	20 (42.6)	37 (75.5)	0.001
pAKT			
Negative	13 (28.9)	19 (38.8)	
Positive	32 (71.1)	30 (61.2)	0.312
pmTor			
Negative	30 (63.8)	33 (67.3)	
Positive	17 (36.2)	16 (32.7)	0.717
pS6			
Negative	22 (47.8)	28 (57.1)	
Positive	24 (52.2)	21 (42.9)	0.183
PTEN			
Negative	18 (38.3)	37 (82.2)	
Positive	29 (61.7)	8 (17.8)	<0.001

doi:10.1371/journal.pone.0141253.t003

was cytoplasmic and, in occasional cases, nuclear. In urothelium with apparent normal histology pmTOR expression was restricted to superficial cell layers. In NMIBC pmTOR expression was evenly distributed across the several layers of urothelial cells, although there was a more intense staining in the superficial layers (Fig 4C). Moreover, several areas with variable staining intensity were observed, denoting a heterogeneous expression. In MIBC positives cases, pmTOR expression was focal and heterogeneous (Fig 4D). pS6 immunoreactivity was predominantly cytoplasmic. In NMIBC pS6 expression was noted in all the superficial layers, both in umbrella and differentiated cells (Fig 4E). The immunoreactivity of pS6 varied across the tumour cells. In MIBC pS6 presented a diffuse expression throughout the tumour, being more present in basal and mitotic cells (Fig 4F). Several positive cases presented increased pS6 staining intensity in the invasion front as well as pS6 expression in tumour infiltrating lymphocytes and endothelial cells.

Taking into account the extension of staining and its intensity, 62/94 (66%), 33/96 (34%) and 45/95 (47%) of the bladder tumours were considered positive for pAkt, pmTOR and pS6, respectively. A Spearman rho test showed that pAkt, pmTOR, pS6 expressions were significantly correlated ($P<0.05$) irrespectively of the tumour stage, thus in accordance with a fully active pathway. Furthermore, despite histological differences, these markers presented an equal distribution among the NMIBC and MIBC and could not be associated with muscle invasion (Table 3).

On the other hand, 37/92 (40%) of the tumours were considered positive for PTEN. PTEN was expressed in the cytoplasm and nucleus of the same cells, however with lower extension of expression in MIBC (33%, Fig 4G) compared to NMIBC (83%; Fig 4H). Moreover, the PTEN-negative phenotype was significantly associated with muscle invasion (Ta and T1; $p<0.001$, Table 3), which may contribute to maintain an active PI3K/Akt/mTOR/S6 pathway in these cases.

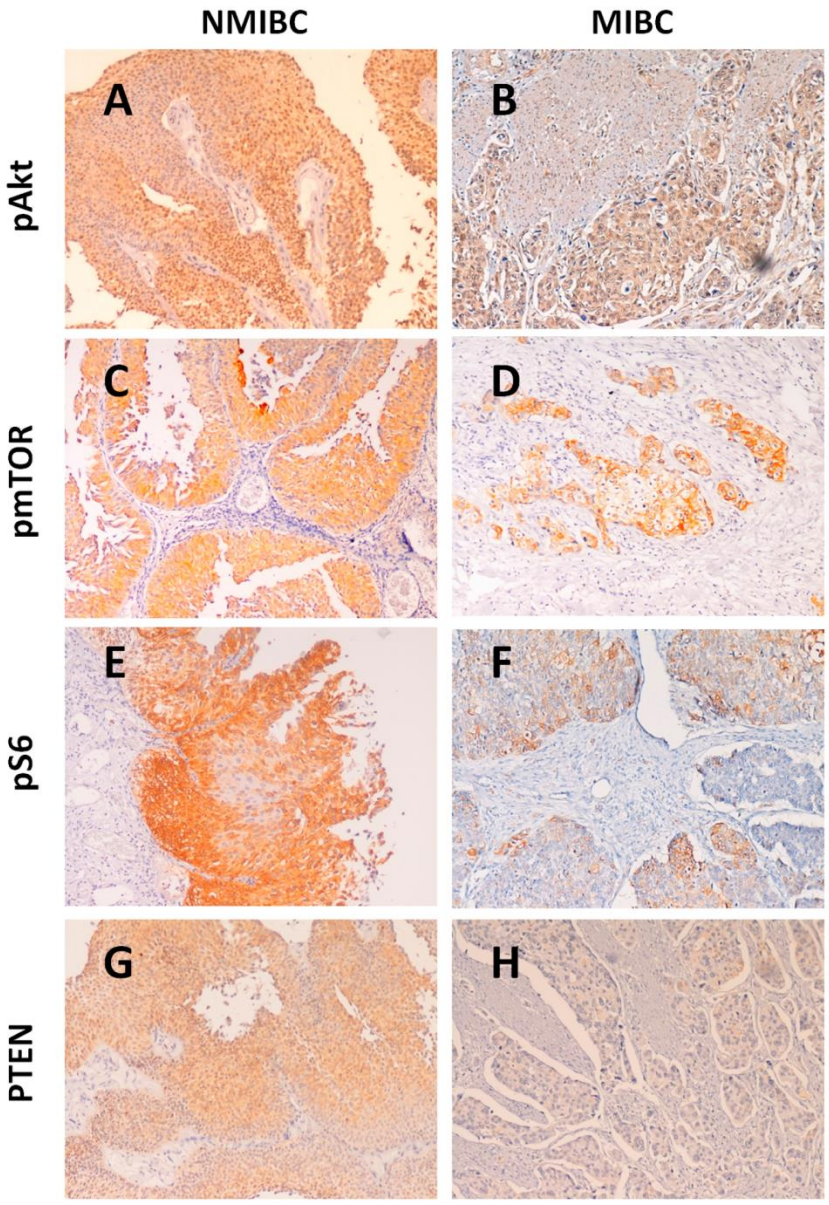


Fig 4. Expressions of pAkt, pmTOR, pS6 and PTEN in NMIBC and MIBC (40x magnification). A and B) pAKT nuclear and cytoplasmatic expression in NMIBC (A) and MIBC (B). In NMIBC cases pAkt presented a heterogeneous pattern with areas of different intensity of expression. In MIBC, stromal cells mainly in the areas close to the tumour showed higher expression. C and D) pmTOR cytoplasmic expression in NMIBC (C) and MIBC (D). In NMIBC pmTOR was expressed across several layers, although there was a more intense staining in the superficial ones. In MIBC positive cases pmTOR expression was focal. E and F) pS6 cytoplasmatic expression in NMIBC (E) and MIBC (F). In NMIBC pS6 expression was observed in all the superficial layers both in umbrella and differentiated cells. In MIBC the immunoreactivity was diffuse, however more present in basal and mitotic cells. pS6 expression was higher in the invasion front and in tumour infiltrating lymphocytes and endothelial cells. G and H) PTEN cytoplasmic and nuclear expressions in NMIBC (G) and MIBC (H). PTEN expression was higher in NMIBC compared to MIBC.

doi:10.1371/journal.pone.0141253.g004

Tn, STn, PI3K/Akt/mTOR pathway and Cancer-specific Survival

A Kaplan-Meier analysis was used to evaluate associations between the addressed biomarkers and the cancer-specific survival of patients. We observed that patients bearing STn expressing tumours had a lower CSS, irrespectively of their stage ($p = 0.024$; Fig 5A). This was also observed when evaluating NMIBC alone ($p = 0.020$; Fig 5B). More importantly, among NMIBC, STn expressing T1 tumours presented lower CSS than negative tumours ($p < 0.05$). Moreover, multivariate Cox regression analysis adjusted to potential confounders, namely age, gender, stage, grade, recurrence status, presence of concomitant CIS was performed. We found that STn is an independent prognostic marker of worst CSS (HR = 11.836; 95%CI: [1.063–131.7]; $p = 0.044$). Contrasting with STn, positive Tn, pAkt, pmTOR and pS6 tumours showed no differences in CSS compared to negative lesions, irrespectively of their stage. We have also observed that patients harbouring PTEN-negative tumours had lower CSS ($p = 0.015$, Fig 6). More studies are necessary to determine if the lack of suppressive effect of PTEN over PI3K/Akt/mTOR may account for these findings.

Based on these observations and aiming to improve the prognostic value of STn in the context of late stage disease (MIBC), we have comprehensively integrated the information from STn and PI3K/Akt/mTOR pathway biomarkers. According to Fig 7, the introduction of PI3K/Akt/mTOR pathway molecules allowed discriminating STn positive MIBC tumours with worst CSS ($p = 0.027$). Furthermore, multivariate Cox regression analysis (adjusted to age, stage, recurrence status, presence of concomitant CIS and metastasis) revealed that the presence of PI3K/Akt/mTOR pathway molecules in STn+ MIBC is independently associated with approximately 6-fold risk of death by cancer (HR = 5.662; 95%CI: [1.093–29.323]; $p = 0.039$). These observations suggest, for the first time, that the combination of STn and mTOR pathway biomarkers may hold potential to improve the stratification of advanced stage bladder tumours; however corroboration in larger series is mandatory.

Inhibition of the PI3K/Akt/mTOR pathway in animal models

BBN-induced mice bladder tumours mimicking the histology and molecular nature of human cancers [20,21], were screened for STn and pS6, the downstream effector of mTOR pathway. We observed no STn expression in the healthy mice urothelium, in accordance with previous observation for the healthy human bladder [5]. In mice healthy urothelium pS6 expression was below 20%, thus underexpressed when compared with BBN-exposed mice (Fig 8). In the control groups (Group 1 and 3, Fig 8A), the exposure to BBN led to the development of invasive tumours in 70–90% of the studied mice. Concomitantly, 83–100% of the invasive lesions overexpressed the STn antigen and all significantly overexpressed pS6 (Fig 8B). This demonstrated that BBN-induced lesions were able to recapitulate the association between altered glycosylation and an activated PI3K/Akt/mTOR pathway previously observed in advanced stage human tumours. The STn antigen was mainly found in cells adjacent to the basal layer and in those invading the stroma, as previously observed in human tumours (Fig 8B and 8C). Conversely, pS6 presented a more diffuse expression, again in accordance with the pattern observed in human lesions (Fig 8B and 8C). A comparison between groups 1 and 3 further highlighted that extended lifespan did not alter the number of invasive lesions, but significantly increased STn and pS6 overall expressions in each tumour ($p < 0.05$; Fig 8B), highlighting the more aggressive nature of Group 3 lesions.

In the sirolimus-treated groups (Groups 2 and 4; Fig 8A) a smaller number of mice developed invasive tumors (20–40%) when compared to the controls (Groups 1 and 3). Moreover, only 43% of the mice treated with sirolimus overexpressed the STn antigen, irrespectively of the experience periods. Still, the extension of STn expression was significantly decreased in

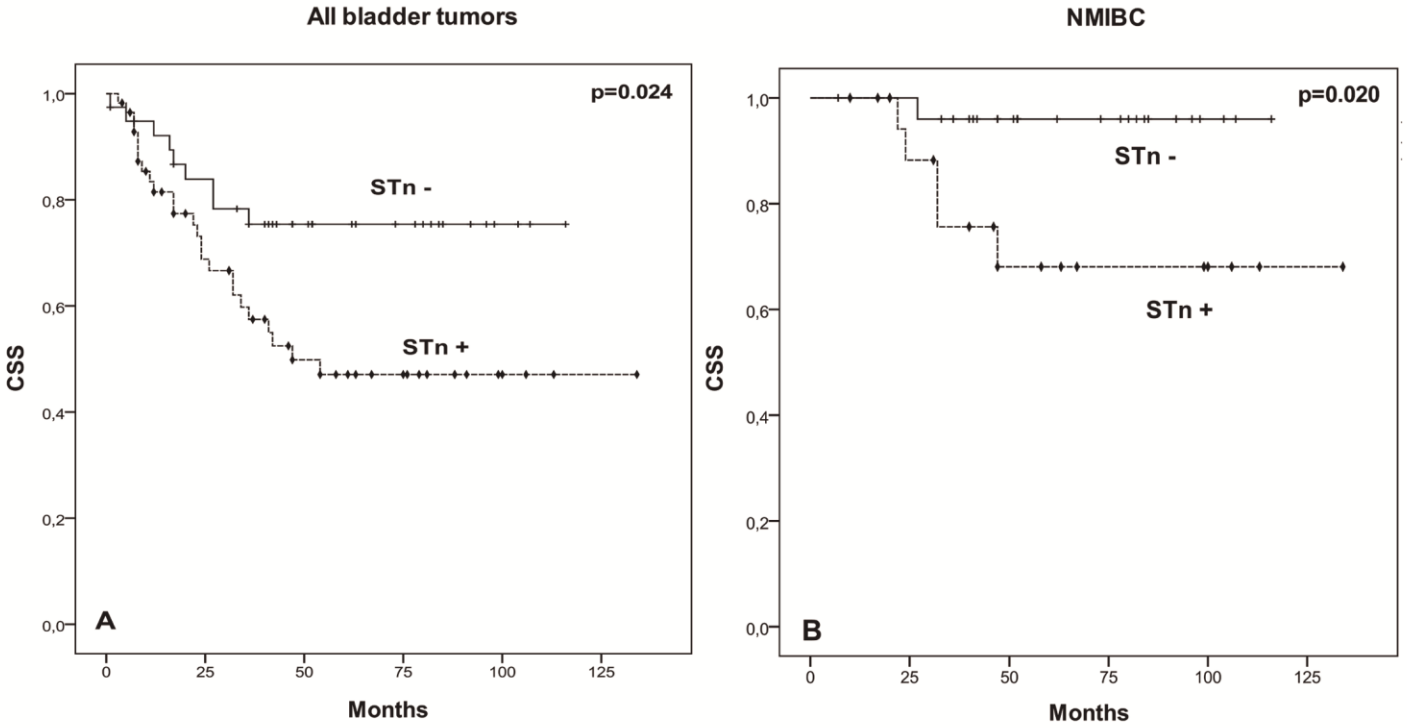


Fig 5. Effect of STn expression in cancer-specific survival (CSS). Kaplan–Meier analysis showing the association between STn and CSS in: (A) all studied bladder cancer patients; (B) NMIBC patients. Comparison performed by log-rank test (A: p = 0.024; B: p = 0.020); + censored STn negative tumours; ♦ censored STn positive tumours.

doi:10.1371/journal.pone.0141253.g005

STn-positive tumours when compared to the control groups (Fig 8B and 8C). Following the same tendency, the pS6 protein was only overexpressed in 29% of the cases in Group 2 and the extension of expression was also significantly decreased (Fig 8B and 8C). Contrastingly, the expression of pS6 in Group 4 was higher than in Group 2, again translating the higher aggressive nature of tumours obtained after longer lifespan. Despite these observations, sirolimus treatment promoted a significant reduction in the percentage of positive pS6 cells in Group 4 mice when compared to Group 3 ($p<0.05$; Fig 8B and 8C). Altogether, sirolimus administration effectively reduced tumour burden and promoted a significant reduction in the expression of STn and pS6 markers.

Discussion

Due to their high molecular heterogeneity, advanced stage bladder tumours present a significant prognostication and treatment hurdle. In this context, much controversy exists regarding the potential of conventional cancer biomarkers, urging the identification of novel molecules capable of aiding disease personalization. Furthermore, advanced stage bladder cancer remains an orphan disease in terms of therapeutics, as the only available options continue to be surgery and conventional chemotherapy [22]. The introduction of targeted therapeutics is therefore warranted.

In a previous explorative study we have observed that altered protein glycosylation translated by STn overexpression was a salient feature of a subset of advanced stage tumours [5]. Herein we have started by investigating the expression of STn precursor, the Tn antigen, in bladder tumours. We observed that this antigen presented a very low expression in bladder

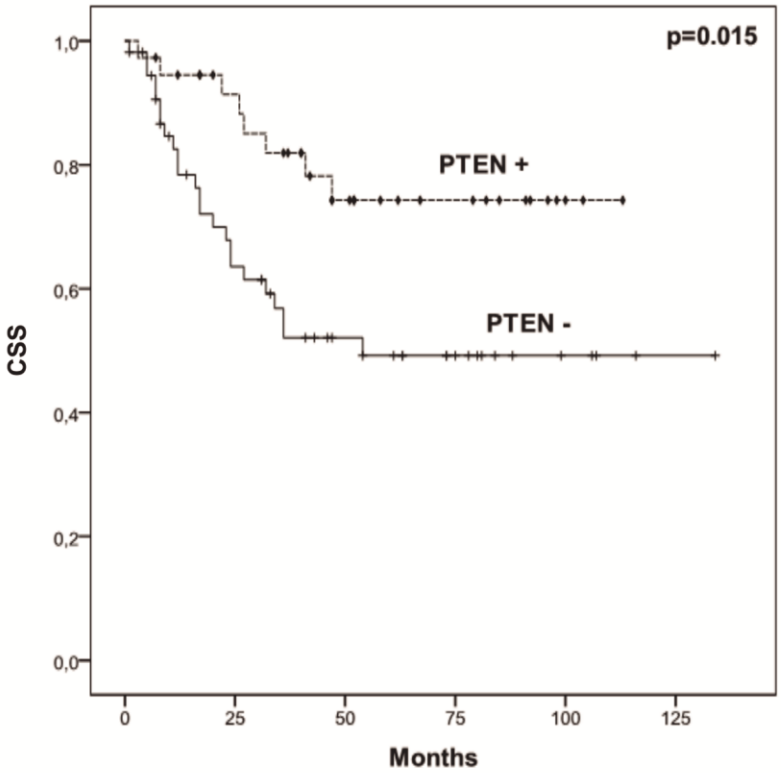


Fig 6. Effect of PTEN expression and cancer-specific survival (CSS) in the studied patients. Kaplan-Meier analysis showing the effect in CSS of PTEN expression in all studied bladder cancer patients. Comparison performed by log-rank test (p = 0.013); + censored PTEN negative tumours; ♦ censored PTEN positive tumours.

doi:10.1371/journal.pone.0141253.g006

tumours and was not associated with any particular stage of the disease. These findings suggest that the Tn antigen is rapidly sialylated or capped with more extended glycans in bladder tumours. Moreover, we have confirmed that STn expression is more associated with muscle invasive than non-muscle invasive disease in a larger patient set, suggesting that sialylation plays a key role in stopping protein glycosylation in advanced stage bladder tumours. Furthermore, we have provided new insights regarding its correlation with decreased survival, as previously observed for digestive track tumours [23–25]. Accordingly, we and other authors have shown that STn expression is responsible by the modulation of cell surface glycoprotein functions in ways that favour malignant phenotypes in gastric [26], breast [27] and bladder [5] cancers. Namely, STn expression altered the adhesive properties of cancer cells, possibly by impairing integrin function [26,27]. Furthermore, it enhanced cell motility, invasion [26,27] and epithelial-to-mesenchymal transition, a key event leading to metastasis [28]. We have also demonstrated that STn expression protects bladder cancer cells from adverse host immune responses [6]. Namely, it impaired dendritic cell maturation inducing a tolerogenic phenotype and limiting their capacity to trigger protective anti-tumour T-cell responses [6]. In resume, a significant amount of data supports a key role of STn in disease progression and dissemination, making of STn antigen, and in particular STn-glycoproteins, potential anti-cancer targets. Nevertheless, there is scarce information about the molecular nature of this subset of STn-expressing aggressive tumours and consequently about the best therapeutic options.

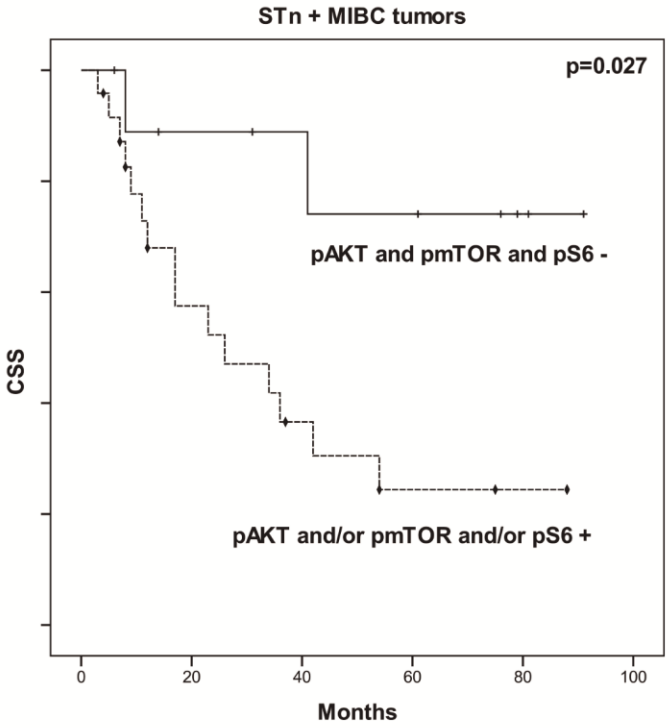


Fig 7. Effect of PI3K/Akt/mTOR pathway activation in cancer-specific survival (CSS) of patients with STn positive MIBC. Kaplan–Meier analysis showing the association between pAKT, pmTOR and pS6 expressions in the CSS of STn positive tumors MIBC: Comparison performed by log-rank test (p = 0.027); + censored pAKT and pmTOR and pS6 negative tumours; ♦ censored pAKT and/or pmTOR and/or pS6 positive tumours.

doi:10.1371/journal.pone.0141253.g007

Foreseeing a more accurate patient stratification we have also addressed the expression of PI3K/Akt/mTOR pathway markers in bladder tumours. In our series the activation of mTOR pathway proteins did not discriminate the stage of disease. Moreover it did not allow, by itself, the identification of patients facing worst prognosis, which is in accordance with recent publications [29,30]. However, we found that PTEN expression, which exerts a suppressive effect over the PI3K/Akt/mTOR pathway, was decreased in advanced stage tumours, in accordance with previous observations [31–34]. Furthermore, PTEN-negative MIBC presented worst cancer-specific survival in comparison to PTEN-positive lesions. More studies are needed to determine if the lack of suppressive effect over the PI3K/Akt/mTOR may account for poorer outcome. Interestingly, we have also observed that the overexpression of PI3K/Akt/mTOR pathway biomarkers decisively associated with worst CSS in STn positive advanced stage tumours, which currently lack effective therapeutics. These findings lead us to hypothesize that this subset of more aggressive bladder tumours may benefit from multi-targeted approaches combining mTOR-inhibitors and guided therapeutics against STn-expressing cells. However these are preliminary insights from a relatively low number of patients. More studies involving a large population are warranted to confirm these observations. It will also be important to evaluate other outcomes of aggressiveness, namely response to conventional therapeutics and metastasis development.

Our study also reinforced that bladder tumours present extensive activation of the PI3K/Akt/mTOR pathway irrespectively of their histological nature, as described in previous publications [32,35]. Such findings contribute to support the idea that most bladder tumours may be good candidates for mTOR-inhibitors therapeutics. Accordingly, mTOR-inhibitors have been

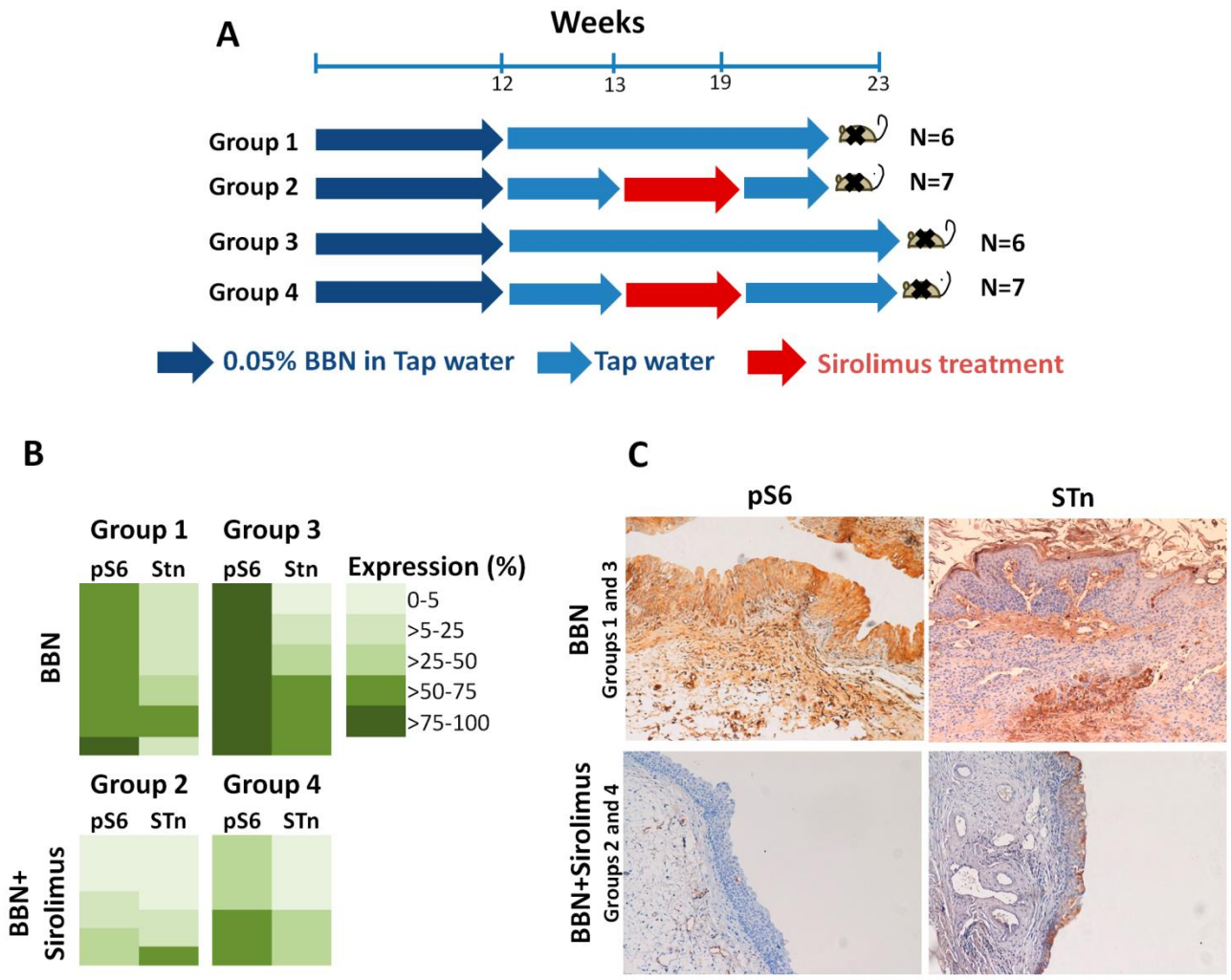


Fig 8. STn and pS6 expressions in bladder tumours from BBN-exposed male ICR mice with or without the administration of mTOR-inhibitor sirolimus (rapamycin). A) Experimental design to determine the sirolimus effect on STn and pS6 expressions in a model of urothelial carcinogenesis (male ICR mice). B) Expression of STn and pS6 in BBN-derived urothelial tumours in the presence and absence of sirolimus. BBN-induced bladder tumours (Groups 1 and 3) overexpressed STn and pS6, which was more pronounced in Group 3, after longer lifespan. Exposure to sirolimus decreased the number of invasive lesions in groups 2 and 4 (data not shown) and, concomitantly, decreased the expressions of STn and pS6. C) Histological sections showing the expressions of STn and pS6 in BBN-induced urothelial tumours before and after treatment.

doi:10.1371/journal.pone.0141253.g008

extensively explored in pre-clinical settings and two phase I/II clinical trials for bladder cancer are ongoing [36]. In particular our group has demonstrated that the combination of everolimus with cisplatin or gemcitabine decreased the proliferation of bladder cancer cell lines in comparison to the chemotherapy agent alone [14,37]. More recently we conducted studies in mice bearing chemically-induced tumours mimicking the histological and molecular nature of human tumours [20]. We concluded that administration of mTOR-pathway inhibitor sirolimus (rapamycin) effectively reduced the frequency of invasive lesions. Using the same animal model, we have now confirmed the anti-cancer activity of sirolimus in the context of aggressive bladder disease. Namely, we observed a significant reduction in tumour burden accompanied by a loss of pS6 expression, thus in accordance with the expected mechanism of action of the drug. Moreover, we are describing for the first time that chemically-induced bladder tumours expressed the

STn antigen, thereby mimicking the glycosylation pattern of human cancers. These observations are of particular importance due the lack of accurate models to access the biological role of this antigen. In fact most established cancer cell lines express residual amounts of this antigen, denoting a dependence on the tumours microenvironment. We believe that BBN-induced tumours may now constitute key models to develop successful therapeutics against STn positive bladder lesions. Moreover importantly, we have concluded that the administration of sirolimus contributed to reduce the number of STn positive cells. These observations reinforce a possible association between STn and an active PI3K/Akt/mTOR pathway in invasive tumours, as suggested upon the evaluation of human cancers. It also points out that sirolimus may constitute a valuable approach to manage STn and PI3K/Akt/mTOR-positive, which face worst OS. Still, these preliminary evidences and more in depth studies are needed before progressing to clinical phases. Namely, it will be important to support these findings in other models such as patient-derived xenografts and compare the effect of sirolimus with conventional chemotherapeutics for bladder cancer (cisplatin/gemcitabine-based regimens).

In resume, we have demonstrated that the STn antigen is a biomarker of poor prognosis, particularly in MIBC. We also suggest the existence of potentially more aggressive subgroup of STn positive MIBC characterized by an active mTOR-pathway. Such observations also provide the first link between these two apparently unrelated events in bladder cancer (altered glycosylation and the PI3K/Akt/mTOR-pathway activation). Using animal models we have also concluded that the administration of mTOR-pathway inhibitor sirolimus offers potential against these highly malignant tumours. More validation studies are now warranted to set the pace for clinical trials. Taking into consideration its cell-surface nature and key role played by STn malignancy, specific antibody-based therapeutics can also be envisaged [22,38]. The combination of these approaches may provide novel ways to improve MIBC management, which remains an orphan disease in terms of innovative treatments [22].

Acknowledgments

This work was supported by Portuguese Foundation for Science and Technology (FCT) Post-doctoral grants SFRH/BPD/66288/2009 (José Alexandre Ferreira), SFRH/BPD/101827/2014 (Luis Lima), SFRH/BPD/85462/2012 (Rui Gil da Costa) and PhD grants SFRH/BD/103571/2014 (Elisabete Fernandes) and SFRH/BD/111242/2015 (Andreia Peixoto). FCT is co-financed by European Social Fund (ESF) under Human Potential Operation Programme (POPH) from National Strategic Reference Framework (NSRF). The authors also acknowledge financial support from ICBAS-UP (Céu Costa and Sofia Pereira) and the Portuguese Association of Urology/Pfizer prize 2013. The authors also thank Professor Celso Reis (IPATIMUP, UP, Portugal) by kindly providing the anti-STn TKH2 and the anti-Tn IE3 monoclonal antibodies used in this work.

Author Contributions

Conceived and designed the experiments: CC SP LL PO JAF LLS. Performed the experiments: CC SP AP EF AT DN MN CG RMGC PO. Analyzed the data: CC SP LL RMGC RC TA PO JAF LLS. Contributed reagents/materials/analysis tools: RC PO JAF LLS. Wrote the paper: LL JAF LLS PO.

References

1. Pasin E, Josephson DY, Mitra AP, Cote RJ, Stein JP. Superficial bladder cancer: an update on etiology, molecular development, classification, and natural history. Rev Urol. 2008; 10: 31–43. PMID: 18470273

2. Babjuk M, Burger M, Zigeuner R, Shariat SF, van Rhijn BWG, Compérat E, et al. EAU guidelines on non-muscle-invasive urothelial carcinoma of the bladder: update 2013. Eur Urol. 2013; 64: 639–53. doi: 10.1016/j.eururo.2013.06.003 PMID: 23827737
3. Miakhil I, Parker SG, Kommu SS, Nethercliffe J. A review of molecular biomarkers for bladder cancer. Int J Med Biomed Res. 2013; 2: 186–194.
4. Dovedi SJ, Davies BR. Emerging targeted therapies for bladder cancer: a disease waiting for a drug. Cancer Metastasis Rev. 2009; 28: 355–67. doi: 10.1007/s10555-009-9192-9 PMID: 19997963
5. Ferreira JA, Videira PA, Lima L, Pereira S, Silva M, Carrascal M, et al. Overexpression of tumour-associated carbohydrate antigen sialyl-Tn in advanced bladder tumours. Mol Oncol. 2013; 7: 719–31. doi: 10.1016/j.molonc.2013.03.001 PMID: 23567325
6. Carrascal MA, Severino PF, Guadalupe Cabral M, Silva M, Ferreira JA, Calais F, et al.Sialyl Tn-expressing bladder cancer cells induce a tolerogenic phenotype in innate and adaptive immune cells. Mol Oncol. 2014; 8: 753–65. doi: 10.1016/j.molonc.2014.02.008 PMID: 24656965
7. Dall'Olio F, Malagolini N, Trinchera M, Chiricolo M. Mechanisms of cancer-associated glycosylation changes. Front Biosci (Landmark Ed). 2012; 17: 670–99.
8. Ma H, Zhou H, Song X, Shi S, Zhang J, Jia L. Modification of sialylation is associated with multidrug resistance in human acute myeloid leukemia. Oncogene. 2015; 34: 726–40. doi: 10.1038/onc.2014.7 PMID: 24531716
9. Porta C, Paglino C, Mosca A. Targeting PI3K/Akt/mTOR Signaling in Cancer. Front Oncol. 2014; 4: 1–11.
10. Ching CB, Hansel DE. Expanding therapeutic targets in bladder cancer: the PI3K/Akt/mTOR pathway. Lab Invest. Nature Publishing Group; 2010; 90: 1406–1414.
11. Wu X, Obata T, Khan Q, Highshaw RA, De Vere White R, Sweeney C. The phosphatidylinositol-3 kinase pathway regulates bladder cancer cell invasion. BJU Int. 2004; 93: 143–150. PMID: 14678387
12. Keniry M, Parsons R. The role of PTEN signaling perturbations in cancer and in targeted therapy. Oncogene. 2008; 27: 5477–5485. doi: 10.1038/onc.2008.248 PMID: 18794882
13. Tamura M, Gu J, Tran H, Yamada KM. PTEN gene and integrin signaling in cancer. J Natl Cancer Inst. 1999; 91: 1820–1828. PMID: 10547389
14. Pinto-Leite R, Arantes-Rodrigues R, Palmeira C, Gaivão I, Cardoso ML, Colaço A, et al. Everolimus enhances gemcitabine-induced cytotoxicity in bladder-cancer cell lines. J Toxicol Env Heal A. 2012; 75: 788–99.
15. Munari E, Fujita K, Faraj S, Chaux A, Gonzalez-Roibon N, Hicks J, et al. Dysregulation of mammalian target of rapamycin pathway in upper tract urothelial carcinoma. Hum Pathol. Elsevier Inc.; 2013; 44: 2668–2676.
16. Nishikawa M, Miyake H, Behnsawy HM, Fujisawa M. Significance of 4E-binding protein 1 as a therapeutic target for invasive urothelial carcinoma of the bladder. Urol Oncol. 2015; 33: 166.e9–15.
17. Chaux A, Compérat E, Varinot J, Hicks J, Lecksell K, Solus J, et al. High levels of phosphatase and tensin homolog expression are associated with tumor progression, tumor recurrence, and systemic metastases in pt1 urothelial carcinoma of the bladder: A tissue microarray study of 156 patients treated by transurethral resect. Urology. 2013; 81: 116–122. doi: 10.1016/j.urology.2012.09.007 PMID: 23273076
18. Oliveira PA, Arantes-Rodrigues R, Sousa-Diniz C, Colaço A, Lourenço L, De La Cruz P LF, et al. The effects of sirolimus on urothelial lesions chemically induced in ICR mice by BBN. Anticancer Res. 2009; 29: 3221–3226. PMID: 19661338
19. Lima L, Severino PF, Silva M, Miranda A, Tavares A, Pereira S et al. Response of high-risk of recurrence/progression bladder tumours expressing sialyl-Tn and sialyl-6-T to BCG immunotherapy. Br J Cancer. 2013; 109: 2106–14. doi: 10.1038/bjc.2013.571 PMID: 24064971
20. Vasconcelos-Nóbrega C, Colaço A, Lopes C, Oliveira PA. BBN as an urothelial carcinogen. In Vivo (Brooklyn). 2012; 26: 727–739.
21. Palmeira C, Oliveira PA, Lameiras C, Amaro T, Silva VM, Lopes C, et al. Biological similarities between murine chemical-induced and natural human bladder carcinogenesis. Oncol Lett. 2010; 1: 373–377. PMID: 22966311
22. Azevedo R, Ferreira JA, Peixoto A, Neves M, Sousa N, Lima A et al. Emerging antibody-based therapeutic strategies for bladder cancer: A systematic review. J Control Release. 2015;
23. Flucke U, Zirbes T, Schröder W, Mönig S, Koch V, Schmitz K, et al. Expression of mucin-associated carbohydrate core antigens in esophageal squamous cell carcinomas. Anticancer Res. 2001; 21: 2189–2193. PMID: 11501845
24. Victorzon M, Nordling S, Nilsson O, Roberts P, Haglund C. Sialyl Tn antigen is an independent predictor of outcome in patients with gastric cancer. Int J Cancer. 1996; 65: 295–300. PMID: 8575847

25. Tsuchiya A, Kikuchi Y, Ando Y, Abe R. Correlation between expression of sialosyl-T antigen and survival in patients with gastric cancer. Br J Surg. 1995; 82: 960–962. PMID: 7648120

26. Pinho S, Marcos NT, Ferreira B, Carvalho AS, Oliveira MJ, Santos-Silva F, et al. Biological significance of cancer-associated sialyl-Tn antigen: modulation of malignant phenotype in gastric carcinoma cells. Cancer Lett. 2007; 249: 157–70. PMID: 16965854

27. Julien S, Adriaenssens E, Ottenberg K, Furlan A, Courtand G, Vercoutter-Edouart AS, et al. ST6GalNAc I expression in MDA-MB-231 breast cancer cells greatly modifies their O-glycosylation pattern and enhances their tumourigenicity. Glycobiology. 2006; 16: 54–64. PMID: 16135558

28. Lin J-C, Liao S-K, Lee E-H, Hung M-S, Sayion Y, Chen H-C, et al. Molecular events associated with epithelial to mesenchymal transition of nasopharyngeal carcinoma cells in the absence of Epstein-Barr virus genome. J Biomed Sci. 2009; 16: 105. doi: 10.1186/1423-0127-16-105 PMID: 19930697

29. Korkolopoulou P, Levidou G, Trigka EA, Prekete N, Karlou M, Thymara I, et al. A comprehensive immunohistochemical and molecular approach to the PI3K/AKT/mTOR (phosphoinositide 3-kinase/v-akt murine thymoma viral oncogene/mammalian target of rapamycin) pathway in bladder urothelial carcinoma. BJU Int. 2012; 110: 1237–1248.

30. Fahmy M, Mansure JJ, Brimo F, Yafi FA, Segal R, Althunayan A, et al. Relevance of the mammalian target of rapamycin pathway in the prognosis of patients with high-risk non–muscle invasive bladder cancer. Hum Pathol. Elsevier Inc.; 2013; 44: 1766–1772.

31. Sun CH, Chang YH, Pan CC. Activation of the PI3K/Akt/mTOR pathway correlates with tumour progression and reduced survival in patients with urothelial carcinoma of the urinary bladder. Histopathology. 2011; 58: 1054–1063. doi: 10.1111/j.1365-2559.2011.03856.x PMID: 21707707

32. Saal LH, Johansson P, Holm K, Gruvberger-Saal SK, She Q-B, Maurer M, et al. Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. Proc Natl Acad Sci U S A. 2007; 104: 7564–7569. PMID: 17452630

33. Harris L, De La Cerda J, Tuziak T, Rosen D, Xiao L, Shen Y, et al. Analysis of the Expression of Biomarkers in Urinary Bladder Cancer Using a Tissue Microarray. Mol Carcinog. 2008; 47: 678–685. doi: 10.1002/mc.20420 PMID: 18288642

34. Calderaro J, Rebouissou S, de Koning L, Masmoudi A, Hérault A, Dubois T, et al. PI3K/AKT pathway activation in bladder carcinogenesis. Int J cancer. 2014; 134: 1776–84. doi: 10.1002/ijc.28518 PMID: 24122582

35. Ferreira J, Bernardo C, Amaro T, Costa C, Lopes P, Silva V, et al. Patient-derived sialyl-Tn positive invasive bladder cancer xenografts in nude mice: An exploratory model study. Eur Urol Suppl. European Association of Urology; 2014; 13: e518.

36. Massari F, Ciccarese C, Santoni M, Brunelli M, Conti A, Modena A, Montironi R, Santini D, Cheng L, Martignoni G, Cascinu S TG. The route to personalized medicine in bladder cancer: where do we stand? Target Oncol. 2015;

37. Kjeldsen T, Clausen H, Hirohashi S, Ogawa T, Iijima H, Hakomori S. Preparation and characterization of monoclonal antibodies directed to the tumor-associated O-linked sialosyl-2——6 alpha-N-acetylgalactosaminyl (sialosyl-Tn) epitope. Cancer Res. 1988; 48: 2214–2220. PMID: 2450649

38. Fernandes E and Ferreira JA, Andreia P, Luís L, Barroso S, Sarmento B, et al. New trends in guided nanotherapies for digestive cancers: A systematic review. J Control Release. 2015; 209: 288–307. doi: 10.1016/j.jconrel.2015.05.003 PMID: 25957905

Appendix B

Table VI. Proteins identified with high confidence level in Tn-negative, blood group A negative, STn-positive basal-like chemoresistant tumors recovered from formalin-fixed paraffin embedded tissues.

Accession	Description
O14874	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Homo sapiens GN=BCKDK PE=1 SV=2 - [BCKD_HUMAN]
Q15118	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial OS=Homo sapiens GN=PDK1 PE=1 SV=1 - [PDK1_HUMAN]
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1 - [1433Z_HUMAN]
Q9NRZ7	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma OS=Homo sapiens GN=AGPAT3 PE=1 SV=1 - [PLCC_HUMAN]
Q9Y2I7	1-phosphatidylinositol 3-phosphate 5-kinase OS=Homo sapiens GN=PIKFYVE PE=1 SV=3 - [FYV1_HUMAN]
Q00722	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 OS=Homo sapiens GN=PLCB2 PE=1 SV=2 - [PLCB2_HUMAN]
Q9BRC7	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-4 OS=Homo sapiens GN=PLCD4 PE=2 SV=1 - [PLCD4_HUMAN]
P16885	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 OS=Homo sapiens GN=PLCG2 PE=1 SV=4 - [PLCG2_HUMAN]
Q6L8Q7	2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2 - [PDE12_HUMAN]
Q9NYL5	24-hydroxycholesterol 7-alpha-hydroxylase OS=Homo sapiens GN=CYP39A1 PE=2 SV=2 - [CP39A_HUMAN]
P29728	2'-5'-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=3 - [OAS2_HUMAN]
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 - [PSMD1_HUMAN]
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]
Q16401	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3 - [PSMD5_HUMAN]
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]
P82664	28S ribosomal protein S10, mitochondrial OS=Homo sapiens GN=MRPS10 PE=1 SV=2 - [RT10_HUMAN]
P82912	28S ribosomal protein S11, mitochondrial OS=Homo sapiens GN=MRPS11 PE=1 SV=2 - [RT11_HUMAN]
P82650	28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1 - [RT22_HUMAN]
Q92552	28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3 - [RT27_HUMAN]
P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]
Q9H0U6	39S ribosomal protein L18, mitochondrial OS=Homo sapiens GN=MRPL18 PE=1 SV=1 - [RM18_HUMAN]
Q9P0M9	39S ribosomal protein L27, mitochondrial OS=Homo sapiens GN=MRPL27 PE=1 SV=1 - [RM27_HUMAN]
Q9BYD2	39S ribosomal protein L9, mitochondrial OS=Homo sapiens GN=MRPL9 PE=1 SV=2 - [RM09_HUMAN]
P04035	3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Homo sapiens GN=HMGCR PE=1 SV=1 - [HMDH_HUMAN]
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens GN=BDH2 PE=1 SV=2 - [BDH2_HUMAN]
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2 - [HIBCH_HUMAN]
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]

P62857	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 - [RS28_HUMAN]
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]
Q8TD47	40S ribosomal protein S4, Y isoform 2 OS=Homo sapiens GN=RPS4Y2 PE=2 SV=3 - [RS4Y2_HUMAN]
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]
P13196	5-aminolevulinate synthase, nonspecific, mitochondrial OS=Homo sapiens GN=ALAS1 PE=1 SV=2 - [HEM1_HUMAN]
P30939	5-hydroxytryptamine receptor 1F OS=Homo sapiens GN=HTR1F PE=2 SV=1 - [5HT1F_HUMAN]
P28223	5-hydroxytryptamine receptor 2A OS=Homo sapiens GN=HTR2A PE=1 SV=2 - [5HT2A_HUMAN]
Q86UY8	5'-nucleotidase domain-containing protein 3 OS=Homo sapiens GN=NT5DC3 PE=2 SV=1 - [NT5D3_HUMAN]
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]
Q7L2J0	7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1 - [MEPCE_HUMAN]
P58397	A disintegrin and metalloproteinase with thrombospondin motifs 12 OS=Homo sapiens GN=ADAMTS12 PE=1 SV=2 - [ATS12_HUMAN]
Q8WXS8	A disintegrin and metalloproteinase with thrombospondin motifs 14 OS=Homo sapiens GN=ADAMTS14 PE=2 SV=2 - [ATS14_HUMAN]
Q9UNA0	A disintegrin and metalloproteinase with thrombospondin motifs 5 OS=Homo sapiens GN=ADAMTS5 PE=1 SV=2 - [ATS5_HUMAN]
Q9UKP5	A disintegrin and metalloproteinase with thrombospondin motifs 6 OS=Homo sapiens GN=ADAMTS6 PE=2 SV=2 - [ATS6_HUMAN]
Q9P2N4	A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 PE=1 SV=4 - [ATS9_HUMAN]
Q7Z5M8	Abhydrolase domain-containing protein 12B OS=Homo sapiens GN=ABHD12B PE=2 SV=1 - [AB12B_HUMAN]
Q8IZP0	Abl interactor 1 OS=Homo sapiens GN=ABI1 PE=1 SV=4 - [ABI1_HUMAN]
Q8IZT6	Abnormal spindle-like microcephaly-associated protein OS=Homo sapiens GN=ASPM PE=1 SV=2 - [ASPM_HUMAN]
Q04844	Acetylcholine receptor subunit epsilon OS=Homo sapiens GN=CHRNE PE=1 SV=2 - [ACHE_HUMAN]
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]
Q9NUB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial OS=Homo sapiens GN=ACSS1 PE=1 SV=2 - [ACS2L_HUMAN]
Q9NR19	Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2 PE=1 SV=1 - [ACSA_HUMAN]
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1 - [AN32A_HUMAN]
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1 - [AN32E_HUMAN]
P10323	Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4 - [ACRO_HUMAN]
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]
O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]
Q8N3C0	Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3 - [ASCC3_HUMAN]
Q6VMQ6	Activating transcription factor 7-interacting protein 1 OS=Homo sapiens GN=ATF7IP PE=1 SV=3 - [MCAF1_HUMAN]
Q9NUZ1	Acyl-coenzyme A oxidase-like protein OS=Homo sapiens GN=ACOXL PE=2 SV=3 - [ACOXL_HUMAN]
P0C7M7	Acyl-coenzyme A synthetase ACSM4, mitochondrial OS=Homo sapiens GN=ACSM4 PE=2 SV=1 - [ACSM4_HUMAN]
Q8WYK0	Acyl-coenzyme A thioesterase 12 OS=Homo sapiens GN=ACOT12 PE=1 SV=1 - [ACO12_HUMAN]
P28039	Acyloxyacyl hydrolase OS=Homo sapiens GN=AOAH PE=1 SV=1 - [AOAH_HUMAN]
Q8N6G6	ADAMTS-like protein 1 OS=Homo sapiens GN=ADAMTSL1 PE=1 SV=4 - [ATL1_HUMAN]
O43734	Adapter protein CIKS OS=Homo sapiens GN=TRAF3IP2 PE=1 SV=3 - [CIKS_HUMAN]
O95996	Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1 - [APC2_HUMAN]
Q6DHV7	Adenosine deaminase-like protein OS=Homo sapiens GN=ADAL PE=2 SV=2 - [ADAL_HUMAN]
Q96PN6	Adenylate cyclase type 10 OS=Homo sapiens GN=ADCY10 PE=1 SV=3 - [ADCYA_HUMAN]
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [PUR8_HUMAN]

P30520	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3 - [PURA2_HUMAN]
Q01518	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 - [CAP1_HUMAN]
P40123	Adenylyl cyclase-associated protein 2 OS=Homo sapiens GN=CAP2 PE=1 SV=1 - [CAP2_HUMAN]
Q8IWK6	Adhesion G protein-coupled receptor A3 OS=Homo sapiens GN=ADGRA3 PE=1 SV=2 - [AGRA3_HUMAN]
Q8IZF6	Adhesion G-protein coupled receptor G4 OS=Homo sapiens GN=ADGRG4 PE=2 SV=2 - [AGRG4_HUMAN]
P18085	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3 - [ARF4_HUMAN]
Q8N4G2	ADP-ribosylation factor-like protein 14 OS=Homo sapiens GN=ARL14 PE=1 SV=2 - [ARL14_HUMAN]
P51825	AF4/FMR2 family member 1 OS=Homo sapiens GN=AFF1 PE=1 SV=1 - [AFF1_HUMAN]
Q9UHB7	AF4/FMR2 family member 4 OS=Homo sapiens GN=AFF4 PE=1 SV=1 - [AFF4_HUMAN]
P55196	Afadin OS=Homo sapiens GN=MLLT4 PE=1 SV=3 - [AFAD_HUMAN]
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]
Q6ULP2	Aftiphilin OS=Homo sapiens GN=AFTPH PE=1 SV=2 - [AFTIN_HUMAN]
O00468	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5 - [AGRIN_HUMAN]
O43572	A-kinase anchor protein 10, mitochondrial OS=Homo sapiens GN=AKAP10 PE=1 SV=2 - [AKA10_HUMAN]
Q9UKA4	A-kinase anchor protein 11 OS=Homo sapiens GN=AKAP11 PE=1 SV=1 - [AKA11_HUMAN]
Q12802	A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 PE=1 SV=2 - [AKP13_HUMAN]
O75969	A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2 - [AKAP3_HUMAN]
Q5JQC9	A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1 - [AKAP4_HUMAN]
Q99996	A-kinase anchor protein 9 OS=Homo sapiens GN=AKAP9 PE=1 SV=3 - [AKAP9_HUMAN]
Q9NQ31	A-kinase-interacting protein 1 OS=Homo sapiens GN=AKIP1 PE=1 SV=2 - [AKIP1_HUMAN]
P43353	Aldehyde dehydrogenase family 3 member B1 OS=Homo sapiens GN=ALDH3B1 PE=1 SV=1 - [AL3B1_HUMAN]
P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]
C9JRZ8	Aldo-keto reductase family 1 member B15 OS=Homo sapiens GN=AKR1B15 PE=1 SV=2 - [AK1BF_HUMAN]
Q9UM73	ALK tyrosine kinase receptor OS=Homo sapiens GN=ALK PE=1 SV=3 - [ALK_HUMAN]
P10696	Alkaline phosphatase, placental-like OS=Homo sapiens GN=ALPPL2 PE=2 SV=4 - [PPBN_HUMAN]
P05186	Alkaline phosphatase, tissue-nonspecific isozyme OS=Homo sapiens GN=ALPL PE=1 SV=4 - [PPBT_HUMAN]
Q13686	Alkylated DNA repair protein alkB homolog 1 OS=Homo sapiens GN=ALKBH1 PE=1 SV=2 - [ALKB1_HUMAN]
Q7Z6M3	Allergin-1 OS=Homo sapiens GN=MILR1 PE=1 SV=2 - [MILR1_HUMAN]
Q6P4F1	Alpha-(1,3)-fucosyltransferase 10 OS=Homo sapiens GN=FUT10 PE=2 SV=2 - [FUT10_HUMAN]
Q96IU4	Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN]
Q9H553	Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Homo sapiens GN=ALG2 PE=1 SV=1 - [ALG2_HUMAN]
Q9UQ53	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B OS=Homo sapiens GN=MGAT4B PE=1 SV=1 - [MGT4B_HUMAN]
Q3V5L5	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B OS=Homo sapiens GN=MGAT5B PE=1 SV=2 - [MGT5B_HUMAN]
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]
Q9NSC7	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 OS=Homo sapiens GN=ST6GALNAC1 PE=2 SV=1 - [SIA7A_HUMAN]
P54802	Alpha-N-acetylglucosaminidase OS=Homo sapiens GN=NAGLU PE=1 SV=2 - [ANAG_HUMAN]
Q96L96	Alpha-protein kinase 3 OS=Homo sapiens GN=ALPK3 PE=2 SV=2 - [ALPK3_HUMAN]
O75443	Alpha-tectorin OS=Homo sapiens GN=TECTA PE=1 SV=3 - [TECTA_HUMAN]
P51170	Amiloride-sensitive sodium channel subunit gamma OS=Homo sapiens GN=SCNN1G PE=1 SV=4 - [SCNNG_HUMAN]
P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]
P23109	AMP deaminase 1 OS=Homo sapiens GN=AMPD1 PE=1 SV=2 - [AMPD1_HUMAN]
Q01433	AMP deaminase 2 OS=Homo sapiens GN=AMPD2 PE=1 SV=2 - [AMPD2_HUMAN]
P15514	Amphiregulin OS=Homo sapiens GN=AREG PE=1 SV=2 - [AREG_HUMAN]
Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein OS=Homo sapiens GN=APBB1IP PE=1 SV=1 - [AB1IP_HUMAN]
Q92624	Amyloid protein-binding protein 2 OS=Homo sapiens GN=APPBP2 PE=1 SV=2 - [APBP2_HUMAN]
Q8N6M9	AN1-type zinc finger protein 2A OS=Homo sapiens GN=ZFAND2A PE=2 SV=2 - [ZFN2A_HUMAN]
Q8N302	Angiogenic factor with G patch and FHA domains 1 OS=Homo sapiens GN=AGGF1 PE=1 SV=2 - [AGGF1_HUMAN]
Q02763	Angiopoietin-1 receptor OS=Homo sapiens GN=TEK PE=1 SV=2 - [TIE2_HUMAN]

Q9Y264	Angiopoietin-4 OS=Homo sapiens GN=ANGPT4 PE=1 SV=1 - [ANGP4_HUMAN]
P12821	Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1 - [ACE_HUMAN]
Q96Q91	Anion exchange protein 4 OS=Homo sapiens GN=SLC4A9 PE=2 SV=2 - [B3A4_HUMAN]
Q9P0K7	Ankycorbin OS=Homo sapiens GN=RAI14 PE=1 SV=2 - [RAI14_HUMAN]
Q8N961	Ankyrin repeat and BTB/POZ domain-containing protein 2 OS=Homo sapiens GN=ABTB2 PE=2 SV=2 - [ABTB2_HUMAN]
A6NHY2	Ankyrin repeat and death domain-containing protein 1B OS=Homo sapiens GN=ANKDD1B PE=3 SV=3 - [AKD1B_HUMAN]
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [ANKH1_HUMAN]
Q8NFD2	Ankyrin repeat and protein kinase domain-containing protein 1 OS=Homo sapiens GN=ANKK1 PE=2 SV=1 - [ANKK1_HUMAN]
Q92625	Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens GN=ANKS1A PE=1 SV=4 - [ANS1A_HUMAN]
Q96Q27	Ankyrin repeat and SOCS box protein 2 OS=Homo sapiens GN=ASB2 PE=1 SV=1 - [ASB2_HUMAN]
Q6UB99	Ankyrin repeat domain-containing protein 11 OS=Homo sapiens GN=ANKRD11 PE=1 SV=3 - [ANR11_HUMAN]
Q4UJ75	Ankyrin repeat domain-containing protein 20A4 OS=Homo sapiens GN=ANKRD20A4 PE=3 SV=1 - [A20A4_HUMAN]
Q8N2N9	Ankyrin repeat domain-containing protein 36B OS=Homo sapiens GN=ANKRD36B PE=1 SV=4 - [AN36B_HUMAN]
Q5TZF3	Ankyrin repeat domain-containing protein 45 OS=Homo sapiens GN=ANKRD45 PE=1 SV=1 - [ANR45_HUMAN]
Q8WVL7	Ankyrin repeat domain-containing protein 49 OS=Homo sapiens GN=ANKRD49 PE=1 SV=1 - [ANR49_HUMAN]
Q9Y2G4	Ankyrin repeat domain-containing protein 6 OS=Homo sapiens GN=ANKRD6 PE=1 SV=3 - [ANKR6_HUMAN]
Q9BZ19	Ankyrin repeat domain-containing protein 60 OS=Homo sapiens GN=ANKRD60 PE=3 SV=3 - [ANR60_HUMAN]
Q96BM1	Ankyrin repeat domain-containing protein 9 OS=Homo sapiens GN=ANKRD9 PE=2 SV=1 - [ANKR9_HUMAN]
Q01484	Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4 - [ANK2_HUMAN]
Q12955	Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3 - [ANK3_HUMAN]
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]
Q32M45	Anoctamin-4 OS=Homo sapiens GN=ANO4 PE=2 SV=1 - [ANO4_HUMAN]
P23352	Anosmin-1 OS=Homo sapiens GN=KAL1 PE=1 SV=3 - [KALM_HUMAN]
P46013	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN]
O00203	AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 - [AP3B1_HUMAN]
Q96N21	AP-4 complex accessory subunit tepsin OS=Homo sapiens GN=ENTHD2 PE=1 SV=1 - [AP4AT_HUMAN]
Q9UPM8	AP-4 complex subunit epsilon-1 OS=Homo sapiens GN=AP4E1 PE=1 SV=2 - [AP4E1_HUMAN]
Q9H0R1	AP-5 complex subunit mu-1 OS=Homo sapiens GN=AP5M1 PE=1 SV=2 - [AP5M1_HUMAN]
Q8N7J2	APC membrane recruitment protein 2 OS=Homo sapiens GN=AMER2 PE=1 SV=3 - [AMER2_HUMAN]
Q0VD83	Apolipoprotein B receptor OS=Homo sapiens GN=APOBR PE=1 SV=2 - [APOBR_HUMAN]
P04114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2 - [APOB_HUMAN]
Q9BPW4	Apolipoprotein L4 OS=Homo sapiens GN=APOL4 PE=2 SV=3 - [APOL4_HUMAN]
Q9BWW9	Apolipoprotein L5 OS=Homo sapiens GN=APOL5 PE=2 SV=1 - [APOL5_HUMAN]
Q96NN9	Apoptosis-inducing factor 3 OS=Homo sapiens GN=AIFM3 PE=1 SV=1 - [AIFM3_HUMAN]
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2 - [ACINU_HUMAN]
Q9NPF8	Arf-GAP with dual PH domain-containing protein 2 OS=Homo sapiens GN=ADAP2 PE=1 SV=1 - [ADAP2_HUMAN]
Q96P48	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3 - [ARAP1_HUMAN]
Q8WZ64	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ARAP2 PE=1 SV=3 - [ARAP2_HUMAN]
Q8WWN8	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=ARAP3 PE=1 SV=1 - [ARAP3_HUMAN]
O00192	Armadillo repeat protein deleted in velo-cardio-facial syndrome OS=Homo sapiens GN=ARVCF PE=1 SV=1 - [ARVC_HUMAN]
Q5W041	Armadillo repeat-containing protein 3 OS=Homo sapiens GN=ARMC3 PE=2 SV=2 - [ARMC3_HUMAN]
Q8NCT1	Arrestin domain-containing protein 4 OS=Homo sapiens GN=ARRDC4 PE=2 SV=3 - [ARRD4_HUMAN]
O00327	Aryl hydrocarbon receptor nuclear translocator-like protein 1 OS=Homo sapiens GN=ARNTL PE=1 SV=2 - [BMAL1_HUMAN]
P15289	Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 - [ARSA_HUMAN]
P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4 - [ASNS_HUMAN]

Q9NWL6	Asparagine synthetase domain-containing protein 1 OS=Homo sapiens GN=ASNSD1 PE=2 SV=2 - [ASND1_HUMAN]
Q6PI48	Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1 - [SYDM_HUMAN]
Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]
O75129	Astrotactin-2 OS=Homo sapiens GN=ASTN2 PE=2 SV=2 - [ASTN2_HUMAN]
O15265	Ataxin-7 OS=Homo sapiens GN=ATXN7 PE=1 SV=1 - [ATX7_HUMAN]
Q14CW9	Ataxin-7-like protein 3 OS=Homo sapiens GN=ATXN7L3 PE=1 SV=1 - [AT7L3_HUMAN]
Q5TGY3	AT-hook DNA-binding motif-containing protein 1 OS=Homo sapiens GN=AHDC1 PE=1 SV=1 - [AHDC1_HUMAN]
Q6DD88	Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1 - [ATLA3_HUMAN]
O43313	ATM interactor OS=Homo sapiens GN=ATMIN PE=1 SV=2 - [ATMIN_HUMAN]
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]
Q96QE3	ATPase family AAA domain-containing protein 5 OS=Homo sapiens GN=ATAD5 PE=1 SV=4 - [ATAD5_HUMAN]
O95477	ATP-binding cassette sub-family A member 1 OS=Homo sapiens GN=ABCA1 PE=1 SV=3 - [ABCA1_HUMAN]
Q8WWZ4	ATP-binding cassette sub-family A member 10 OS=Homo sapiens GN=ABCA10 PE=2 SV=3 - [ABCAA_HUMAN]
Q86UK0	ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=3 - [ABCAC_HUMAN]
O94911	ATP-binding cassette sub-family A member 8 OS=Homo sapiens GN=ABCA8 PE=1 SV=3 - [ABCA8_HUMAN]
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1 - [ABCB6_HUMAN]
O75027	ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens GN=ABCB7 PE=1 SV=2 - [ABCB7_HUMAN]
Q09428	ATP-binding cassette sub-family C member 8 OS=Homo sapiens GN=ABCC8 PE=1 SV=6 - [ABCC8_HUMAN]
O60706	ATP-binding cassette sub-family C member 9 OS=Homo sapiens GN=ABCC9 PE=1 SV=2 - [ABCC9_HUMAN]
Q9H221	ATP-binding cassette sub-family G member 8 OS=Homo sapiens GN=ABCG8 PE=1 SV=1 - [ABCG8_HUMAN]
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]
P08237	ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [PFKAM_HUMAN]
O94761	ATP-dependent DNA helicase Q4 OS=Homo sapiens GN=RECQL4 PE=1 SV=1 - [RECQ4_HUMAN]
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]
Q9GZR7	ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1 - [DDX24_HUMAN]
O15523	ATP-dependent RNA helicase DDX3Y OS=Homo sapiens GN=DDX3Y PE=1 SV=2 - [DDX3Y_HUMAN]
Q9H2U1	ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2 - [DHX36_HUMAN]
Q14562	ATP-dependent RNA helicase DHX8 OS=Homo sapiens GN=DHX8 PE=1 SV=1 - [DHX8_HUMAN]
P16066	Atrial natriuretic peptide receptor 1 OS=Homo sapiens GN=NPR1 PE=1 SV=1 - [ANPRA_HUMAN]
P20594	Atrial natriuretic peptide receptor 2 OS=Homo sapiens GN=NPR2 PE=1 SV=1 - [ANPRB_HUMAN]
Q8NFD5	AT-rich interactive domain-containing protein 1B OS=Homo sapiens GN=ARID1B PE=1 SV=2 - [ARI1B_HUMAN]
Q99856	AT-rich interactive domain-containing protein 3A OS=Homo sapiens GN=ARID3A PE=1 SV=2 - [ARI3A_HUMAN]
Q4LE39	AT-rich interactive domain-containing protein 4B OS=Homo sapiens GN=ARID4B PE=1 SV=2 - [ARI4B_HUMAN]
Q14865	AT-rich interactive domain-containing protein 5B OS=Homo sapiens GN=ARID5B PE=1 SV=3 - [ARI5B_HUMAN]
Q5VV63	Attractin-like protein 1 OS=Homo sapiens GN=ATRNL1 PE=2 SV=2 - [ATRN1_HUMAN]
Q9NWT8	Aurora kinase A-interacting protein OS=Homo sapiens GN=AURKAIP1 PE=1 SV=1 - [AKIP_HUMAN]
Q8NAA4	Autophagy-related protein 16-2 OS=Homo sapiens GN=ATG16L2 PE=1 SV=2 - [A16L2_HUMAN]
Q9Y2T1	Axin-2 OS=Homo sapiens GN=AXIN2 PE=1 SV=1 - [AXIN2_HUMAN]
P20160	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3 - [CAP7_HUMAN]
P17213	Bactericidal permeability-increasing protein OS=Homo sapiens GN=BPI PE=1 SV=4 - [BPI_HUMAN]
Q13489	Baculoviral IAP repeat-containing protein 3 OS=Homo sapiens GN=BIRC3 PE=1 SV=2 - [BIRC3_HUMAN]
Q9NR09	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2 - [BIRC6_HUMAN]
Q9P281	BAH and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=BAHCC1 PE=1 SV=3 - [BAHC1_HUMAN]
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3 - [B3AT_HUMAN]

P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2 - [BCAM_HUMAN]
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 - [PGBM_HUMAN]
Q68DE3	Basic helix-loop-helix domain-containing protein KIAA2018 OS=Homo sapiens GN=KIAA2018 PE=1 SV=3 - [K2018_HUMAN]
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1 - [BZW2_HUMAN]
Q8N1L9	Basic leucine zipper transcriptional factor ATF-like 2 OS=Homo sapiens GN=BATF2 PE=1 SV=1 - [BATF2_HUMAN]
Q8WV28	B-cell linker protein OS=Homo sapiens GN=BLNK PE=1 SV=2 - [BLNK_HUMAN]
Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]
Q9BXK5	Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1 - [B2L13_HUMAN]
O76090	Bestrophin-1 OS=Homo sapiens GN=BEST1 PE=1 SV=1 - [BEST1_HUMAN]
Q8N1M1	Bestrophin-3 OS=Homo sapiens GN=BEST3 PE=2 SV=1 - [BEST3_HUMAN]
O95395	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 3 OS=Homo sapiens GN=GCNT3 PE=2 SV=1 - [GCNT3_HUMAN]
Q9P109	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 4 OS=Homo sapiens GN=GCNT4 PE=2 SV=1 - [GCNT4_HUMAN]
Q00973	Beta-1,4 N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=B4GALNT1 PE=1 SV=2 - [B4GN1_HUMAN]
O60512	Beta-1,4-galactosyltransferase 3 OS=Homo sapiens GN=B4GALT3 PE=1 SV=2 - [B4GT3_HUMAN]
Q9UBV7	Beta-1,4-galactosyltransferase 7 OS=Homo sapiens GN=B4GALT7 PE=1 SV=1 - [B4GT7_HUMAN]
P32121	Beta-arrestin-2 OS=Homo sapiens GN=ARRB2 PE=1 SV=2 - [ARRB2_HUMAN]
Q8N687	Beta-defensin 125 OS=Homo sapiens GN=DEFB125 PE=2 SV=2 - [DB125_HUMAN]
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]
Q9HBI1	Beta-parvin OS=Homo sapiens GN=PARVB PE=1 SV=1 - [PARVB_HUMAN]
Q6NYC1	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Homo sapiens GN=JMJD6 PE=1 SV=1 - [JMJD6_HUMAN]
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]
P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]
Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]
P50747	Biotin--protein ligase OS=Homo sapiens GN=HLCS PE=1 SV=1 - [BPL1_HUMAN]
P18577	Blood group Rh(CE) polypeptide OS=Homo sapiens GN=RHCE PE=1 SV=2 - [RHCE_HUMAN]
O60477	BMP/retinoic acid-inducible neural-specific protein 1 OS=Homo sapiens GN=BRINP1 PE=1 SV=2 - [BRNP1_HUMAN]
Q76B58	BMP/retinoic acid-inducible neural-specific protein 3 OS=Homo sapiens GN=BRINP3 PE=1 SV=1 - [BRNP3_HUMAN]
P13727	Bone marrow proteoglycan OS=Homo sapiens GN=PRG2 PE=1 SV=2 - [PRG2_HUMAN]
P13497	Bone morphogenetic protein 1 OS=Homo sapiens GN=BMP1 PE=1 SV=2 - [BMP1_HUMAN]
O95393	Bone morphogenetic protein 10 OS=Homo sapiens GN=BMP10 PE=1 SV=1 - [BMP10_HUMAN]
O95972	Bone morphogenetic protein 15 OS=Homo sapiens GN=BMP15 PE=1 SV=2 - [BMP15_HUMAN]
P12644	Bone morphogenetic protein 4 OS=Homo sapiens GN=BMP4 PE=1 SV=1 - [BMP4_HUMAN]
P80723	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 - [BASP1_HUMAN]
Q8WXS3	Brain and acute leukemia cytoplasmic protein OS=Homo sapiens GN=BAALC PE=2 SV=3 - [BAALC_HUMAN]
Q7Z569	BRCA1-associated protein OS=Homo sapiens GN=BRAP PE=1 SV=2 - [BRAP_HUMAN]
P11274	Breakpoint cluster region protein OS=Homo sapiens GN=BCR PE=1 SV=2 - [BCR_HUMAN]
Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2 - [BIG1_HUMAN]
Q5TH69	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Homo sapiens GN=ARFGEF3 PE=1 SV=3 - [BIG3_HUMAN]
Q9ULD4	Bromodomain and PHD finger-containing protein 3 OS=Homo sapiens GN=BRPF3 PE=1 SV=2 - [BRPF3_HUMAN]
O95696	Bromodomain-containing protein 1 OS=Homo sapiens GN=BRD1 PE=1 SV=1 - [BRD1_HUMAN]
Q9H0E9	Bromodomain-containing protein 8 OS=Homo sapiens GN=BRD8 PE=1 SV=2 - [BRD8_HUMAN]
Q9NW68	BSD domain-containing protein 1 OS=Homo sapiens GN=BSDC1 PE=1 SV=1 - [BSDC1_HUMAN]
Q9H0C5	BTB/POZ domain-containing protein 1 OS=Homo sapiens GN=BTBD1 PE=1 SV=1 - [BTBD1_HUMAN]
Q96Q07	BTB/POZ domain-containing protein 9 OS=Homo sapiens GN=BTBD9 PE=2 SV=2 - [BTBD9_HUMAN]
Q7Z5Y7	BTB/POZ domain-containing protein KCTD20 OS=Homo sapiens GN=KCTD20 PE=1 SV=1 - [KCD20_HUMAN]
Q9Y597	BTB/POZ domain-containing protein KCTD3 OS=Homo sapiens GN=KCTD3 PE=1 SV=2 - [KCTD3_HUMAN]

P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]
O75844	CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2 - [FACE1_HUMAN]
Q8WUQ7	Cactin OS=Homo sapiens GN=CACTIN PE=1 SV=3 - [CATIN_HUMAN]
Q9NYQ6	Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1 - [CELR1_HUMAN]
Q9HCU4	Cadherin EGF LAG seven-pass G-type receptor 2 OS=Homo sapiens GN=CELSR2 PE=1 SV=1 - [CELR2_HUMAN]
Q9NYQ7	Cadherin EGF LAG seven-pass G-type receptor 3 OS=Homo sapiens GN=CELSR3 PE=1 SV=2 - [CELR3_HUMAN]
P55290	Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1 - [CAD13_HUMAN]
Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=2 SV=3 - [CAD17_HUMAN]
P22223	Cadherin-3 OS=Homo sapiens GN=CDH3 PE=1 SV=2 - [CADH3_HUMAN]
P55283	Cadherin-4 OS=Homo sapiens GN=CDH4 PE=2 SV=2 - [CADH4_HUMAN]
Q9ULB5	Cadherin-7 OS=Homo sapiens GN=CDH7 PE=2 SV=2 - [CADH7_HUMAN]
Q6ZTQ4	Cadherin-related family member 3 OS=Homo sapiens GN=CDHR3 PE=1 SV=1 - [CDHR3_HUMAN]
Q99653	Calcineurin B homologous protein 1 OS=Homo sapiens GN=CHP1 PE=1 SV=3 - [CHP1_HUMAN]
P49069	Calcium signal-modulating cyclophilin ligand OS=Homo sapiens GN=CAMLG PE=1 SV=1 - [CAMLG_HUMAN]
Q9BPX6	Calcium uptake protein 1, mitochondrial OS=Homo sapiens GN=MICU1 PE=1 SV=1 - [MICU1_HUMAN]
Q8IU85	Calcium/calmodulin-dependent protein kinase type 1D OS=Homo sapiens GN=CAMK1D PE=1 SV=1 - [KCC1D_HUMAN]
Q9H9S4	Calcium-binding protein 39-like OS=Homo sapiens GN=CAB39L PE=1 SV=3 - [CB39L_HUMAN]
Q9NP86	Calcium-binding protein 5 OS=Homo sapiens GN=CABP5 PE=1 SV=1 - [CABP5_HUMAN]
Q9Y6Y1	Calmodulin-binding transcription activator 1 OS=Homo sapiens GN=CAMTA1 PE=1 SV=4 - [CMTA1_HUMAN]
Q5T5Y3	Calmodulin-regulated spectrin-associated protein 1 OS=Homo sapiens GN=CAMSAP1 PE=1 SV=2 - [CAMP1_HUMAN]
O15484	Calpain-5 OS=Homo sapiens GN=CAPN5 PE=1 SV=2 - [CAN5_HUMAN]
A6NHC0	Calpain-8 OS=Homo sapiens GN=CAPN8 PE=2 SV=3 - [CAN8_HUMAN]
P22612	cAMP-dependent protein kinase catalytic subunit gamma OS=Homo sapiens GN=PRKACG PE=1 SV=3 - [KAPCG_HUMAN]
P61925	cAMP-dependent protein kinase inhibitor alpha OS=Homo sapiens GN=PKIA PE=1 SV=2 - [IPKA_HUMAN]
Q08493	cAMP-specific 3',5'-cyclic phosphodiesterase 4C OS=Homo sapiens GN=PDE4C PE=1 SV=2 - [PDE4C_HUMAN]
Q08499	cAMP-specific 3',5'-cyclic phosphodiesterase 4D OS=Homo sapiens GN=PDE4D PE=1 SV=2 - [PDE4D_HUMAN]
Q92887	Canalicular multispecific organic anion transporter 1 OS=Homo sapiens GN=ABCC2 PE=1 SV=3 - [MRP2_HUMAN]
Q14444	Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 - [CAPR1_HUMAN]
Q6IMN6	Caprin-2 OS=Homo sapiens GN=CAPRIN2 PE=1 SV=1 - [CAPR2_HUMAN]
Q8N1G2	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Homo sapiens GN=CMTR1 PE=1 SV=1 - [CMTR1_HUMAN]
P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]
Q9NPF2	Carbohydrate sulfotransferase 11 OS=Homo sapiens GN=CHST11 PE=1 SV=1 - [CHSTB_HUMAN]
Q8NCH0	Carbohydrate sulfotransferase 14 OS=Homo sapiens GN=CHST14 PE=1 SV=2 - [CHSTE_HUMAN]
Q7LGC8	Carbohydrate sulfotransferase 3 OS=Homo sapiens GN=CHST3 PE=1 SV=3 - [CHST3_HUMAN]
Q8NCG5	Carbohydrate sulfotransferase 4 OS=Homo sapiens GN=CHST4 PE=1 SV=2 - [CHST4_HUMAN]
Q7L1S5	Carbohydrate sulfotransferase 9 OS=Homo sapiens GN=CHST9 PE=2 SV=2 - [CHST9_HUMAN]
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]
P22748	Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2 - [CAH4_HUMAN]
O75052	Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein OS=Homo sapiens GN=NOS1AP PE=1 SV=3 - [CAPON_HUMAN]
P15086	Carboxypeptidase B OS=Homo sapiens GN=CPB1 PE=1 SV=4 - [CBPB1_HUMAN]
O75976	Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2 - [CBPD_HUMAN]
Q9Y646	Carboxypeptidase Q OS=Homo sapiens GN=CPQ PE=1 SV=1 - [CBPQ_HUMAN]
P13688	Carcinoembryonic antigen-related cell adhesion molecule 1 OS=Homo sapiens GN=CEACAM1 PE=1 SV=2 - [CEAM1_HUMAN]
Q8N3K9	Cardiomyopathy-associated protein 5 OS=Homo sapiens GN=CMYA5 PE=1 SV=3 - [CMYA5_HUMAN]
Q8N4J0	Carnosine N-methyltransferase OS=Homo sapiens GN=C9orf41 PE=1 SV=1 - [CARME_HUMAN]
A5YM72	Carnosine synthase 1 OS=Homo sapiens GN=CARNS1 PE=1 SV=3 - [CRNS1_HUMAN]

P48730	Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2 - [KC1D_HUMAN]
Q5EG05	Caspase recruitment domain-containing protein 16 OS=Homo sapiens GN=CARD16 PE=1 SV=1 - [CAR16_HUMAN]
Q9Y2G2	Caspase recruitment domain-containing protein 8 OS=Homo sapiens GN=CARD8 PE=1 SV=1 - [CARD8_HUMAN]
P29466	Caspase-1 OS=Homo sapiens GN=CASP1 PE=1 SV=1 - [CASP1_HUMAN]
Q14790	Caspase-8 OS=Homo sapiens GN=CASP8 PE=1 SV=1 - [CASP8_HUMAN]
O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]
Q9UQB3	Catenin delta-2 OS=Homo sapiens GN=CTNND2 PE=1 SV=3 - [CTND2_HUMAN]
P07858	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 - [CATB_HUMAN]
P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]
P07711	Cathepsin L1 OS=Homo sapiens GN=CTSL PE=1 SV=2 - [CATL1_HUMAN]
Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]
P20645	Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1 - [MPRD_HUMAN]
Q86WG3	Caytaxin OS=Homo sapiens GN=ATCAY PE=1 SV=2 - [ATCAY_HUMAN]
P51684	C-C chemokine receptor type 6 OS=Homo sapiens GN=CCR6 PE=2 SV=2 - [CCR6_HUMAN]
O15444	C-C motif chemokine 25 OS=Homo sapiens GN=CCL25 PE=1 SV=2 - [CCL25_HUMAN]
P49716	CCAAT/enhancer-binding protein delta OS=Homo sapiens GN=CEBPD PE=1 SV=2 - [CEBPD_HUMAN]
Q9H9A5	CCR4-NOT transcription complex subunit 10 OS=Homo sapiens GN=CNOT10 PE=1 SV=1 - [CNO10_HUMAN]
Q01151	CD83 antigen OS=Homo sapiens GN=CD83 PE=1 SV=1 - [CD83_HUMAN]
Q96SN8	CDK5 regulatory subunit-associated protein 2 OS=Homo sapiens GN=CDK5RAP2 PE=1 SV=5 - [CK5P2_HUMAN]
Q8N126	Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1 - [CADM3_HUMAN]
O75943	Cell cycle checkpoint protein RAD17 OS=Homo sapiens GN=RAD17 PE=1 SV=2 - [RAD17_HUMAN]
P30260	Cell division cycle protein 27 homolog OS=Homo sapiens GN=CDC27 PE=1 SV=2 - [CDC27_HUMAN]
P29373	Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=CRABP2 PE=1 SV=2 - [RABP2_HUMAN]
Q12798	Centrin-1 OS=Homo sapiens GN=CETN1 PE=1 SV=1 - [CETN1_HUMAN]
Q7Z7A1	Centriolin OS=Homo sapiens GN=CNTRL PE=1 SV=2 - [CNTRL_HUMAN]
P49454	Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2 - [CENPF_HUMAN]
Q9H3R5	Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1 - [CENPH_HUMAN]
Q96BT3	Centromere protein T OS=Homo sapiens GN=CENPT PE=1 SV=2 - [CENPT_HUMAN]
Q71F23	Centromere protein U OS=Homo sapiens GN=CENPU PE=1 SV=1 - [CENPU_HUMAN]
Q8N960	Centrosomal protein of 120 kDa OS=Homo sapiens GN=CEP120 PE=1 SV=2 - [CE120_HUMAN]
Q66GS9	Centrosomal protein of 135 kDa OS=Homo sapiens GN=CEP135 PE=1 SV=2 - [CP135_HUMAN]
O94986	Centrosomal protein of 152 kDa OS=Homo sapiens GN=CEP152 PE=1 SV=4 - [CE152_HUMAN]
Q5TB80	Centrosomal protein of 162 kDa OS=Homo sapiens GN=CEP162 PE=1 SV=2 - [CE162_HUMAN]
Q8TEP8	Centrosomal protein of 192 kDa OS=Homo sapiens GN=CEP192 PE=1 SV=2 - [CE192_HUMAN]
Q9C0F1	Centrosomal protein of 44 kDa OS=Homo sapiens GN=CEP44 PE=1 SV=2 - [CEP44_HUMAN]
Q86XR8	Centrosomal protein of 57 kDa OS=Homo sapiens GN=CEP57 PE=1 SV=2 - [CEP57_HUMAN]
Q6P2H3	Centrosomal protein of 85 kDa OS=Homo sapiens GN=CEP85 PE=1 SV=1 - [CEP85_HUMAN]
Q5VT06	Centrosome-associated protein 350 OS=Homo sapiens GN=CEP350 PE=1 SV=1 - [CE350_HUMAN]
Q9BV73	Centrosome-associated protein CEP250 OS=Homo sapiens GN=CEP250 PE=1 SV=2 - [CP250_HUMAN]
Q96MC4	CEP295 N-terminal-like protein OS=Homo sapiens GN=CEP295NL PE=2 SV=1 - [C295L_HUMAN]
O95813	Cerberus OS=Homo sapiens GN=CER1 PE=1 SV=1 - [CER1_HUMAN]
Q9NUG4	Cerebral cavernous malformations 2 protein-like OS=Homo sapiens GN=CCM2L PE=2 SV=3 - [CCM2L_HUMAN]
Q9HD42	Charged multivesicular body protein 1a OS=Homo sapiens GN=CHMP1A PE=1 SV=1 - [CHM1A_HUMAN]
Q8NHY5	Checkpoint protein HUS1B OS=Homo sapiens GN=HUS1B PE=1 SV=2 - [HUS1B_HUMAN]
P51788	Chloride channel protein 2 OS=Homo sapiens GN=CLCN2 PE=1 SV=2 - [CLCN2_HUMAN]
Q9Y6A2	Cholesterol 24-hydroxylase OS=Homo sapiens GN=CYP46A1 PE=1 SV=1 - [CP46A_HUMAN]
Q8N4M1	Choline transporter-like protein 3 OS=Homo sapiens GN=SLC44A3 PE=1 SV=4 - [CTL3_HUMAN]
Q8N6G5	Chondroitin sulfate N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=CSGALNACT2 PE=1 SV=1 - [CGAT2_HUMAN]
Q70JA7	Chondroitin sulfate synthase 3 OS=Homo sapiens GN=CHSY3 PE=2 SV=3 - [CHSS3_HUMAN]

P01233	Choriogonadotropin subunit beta OS=Homo sapiens GN=CGB PE=1 SV=1 - [CGHB_HUMAN]
P0DML2	Chorionic somatomammotropin hormone 1 OS=Homo sapiens GN=CSH1 PE=1 SV=1 - [CSH1_HUMAN]
Q13111	Chromatin assembly factor 1 subunit A OS=Homo sapiens GN=CHAF1A PE=1 SV=2 - [CAF1A_HUMAN]
O14646	Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2 - [CHD1_HUMAN]
Q12873	Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3 - [CHD3_HUMAN]
Q14839	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HUMAN]
Q9P2D1	Chromodomain-helicase-DNA-binding protein 7 OS=Homo sapiens GN=CHD7 PE=1 SV=3 - [CHD7_HUMAN]
Q3L8U1	Chromodomain-helicase-DNA-binding protein 9 OS=Homo sapiens GN=CHD9 PE=1 SV=2 - [CHD9_HUMAN]
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens GN=CHAMP1 PE=1 SV=2 - [CHAP1_HUMAN]
Q9P2M7	Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2 - [CING_HUMAN]
Q0VF96	Cingulin-like protein 1 OS=Homo sapiens GN=CGNL1 PE=1 SV=2 - [CGNL1_HUMAN]
Q9ULV3	Cip1-interacting zinc finger protein OS=Homo sapiens GN=CIZ1 PE=1 SV=2 - [CIZ1_HUMAN]
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]
Q8NHS4	Clathrin heavy chain linker domain-containing protein 1 OS=Homo sapiens GN=CLHC1 PE=1 SV=3 - [CLHC1_HUMAN]
Q8N7P3	Claudin-22 OS=Homo sapiens GN=CLDN22 PE=2 SV=3 - [CLD22_HUMAN]
P56747	Claudin-6 OS=Homo sapiens GN=CLDN6 PE=1 SV=2 - [CLD6_HUMAN]
Q10570	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 - [CPSF1_HUMAN]
Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 - [CPSF3_HUMAN]
P33240	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 - [CSTF2_HUMAN]
Q16842	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 2 OS=Homo sapiens GN=ST3GAL2 PE=2 SV=1 - [SIA4B_HUMAN]
Q11206	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 4 OS=Homo sapiens GN=ST3GAL4 PE=2 SV=1 - [SIA4C_HUMAN]
Q8TDQ1	CMRF35-like molecule 1 OS=Homo sapiens GN=CD300LF PE=1 SV=3 - [CLM1_HUMAN]
Q496F6	CMRF35-like molecule 2 OS=Homo sapiens GN=CD300E PE=1 SV=2 - [CLM2_HUMAN]
Q6UXZ3	CMRF35-like molecule 4 OS=Homo sapiens GN=CD300LD PE=1 SV=1 - [CLM4_HUMAN]
Q6UXG3	CMRF35-like molecule 9 OS=Homo sapiens GN=CD300LG PE=1 SV=2 - [CLM9_HUMAN]
Q8N9R6	CMT1A duplicated region transcript 4 protein OS=Homo sapiens GN=CDRT4 PE=2 SV=2 - [CDRT4_HUMAN]
P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4 - [FA5_HUMAN]
P00451	Coagulation factor VIII OS=Homo sapiens GN=F8 PE=1 SV=1 - [FA8_HUMAN]
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 - [COPG1_HUMAN]
Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 - [COPG2_HUMAN]
O43405	Cochlin OS=Homo sapiens GN=COCH PE=1 SV=1 - [COCH_HUMAN]
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]
Q8N3U4	Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=1 SV=3 - [STAG2_HUMAN]
Q6P1N0	Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens GN=CC2D1A PE=1 SV=1 - [C2D1A_HUMAN]
Q8IW40	Coiled-coil domain-containing protein 103 OS=Homo sapiens GN=CCDC103 PE=1 SV=1 - [CC103_HUMAN]
Q6ZU64	Coiled-coil domain-containing protein 108 OS=Homo sapiens GN=CCDC108 PE=1 SV=2 - [CC108_HUMAN]
Q8NEF3	Coiled-coil domain-containing protein 112 OS=Homo sapiens GN=CCDC112 PE=1 SV=2 - [CC112_HUMAN]
Q8WUD4	Coiled-coil domain-containing protein 12 OS=Homo sapiens GN=CCDC12 PE=1 SV=1 - [CCD12_HUMAN]
Q96HB5	Coiled-coil domain-containing protein 120 OS=Homo sapiens GN=CCDC120 PE=1 SV=1 - [CC120_HUMAN]
Q96CT7	Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1 - [CC124_HUMAN]
Q6PK04	Coiled-coil domain-containing protein 137 OS=Homo sapiens GN=CCDC137 PE=1 SV=1 - [CC137_HUMAN]
Q49A88	Coiled-coil domain-containing protein 14 OS=Homo sapiens GN=CCDC14 PE=1 SV=3 - [CCD14_HUMAN]
Q6ZP82	Coiled-coil domain-containing protein 141 OS=Homo sapiens GN=CCDC141 PE=1 SV=2 - [CC141_HUMAN]
Q8NCX0	Coiled-coil domain-containing protein 150 OS=Homo sapiens GN=CCDC150 PE=1 SV=2 - [CC150_HUMAN]
A6NI56	Coiled-coil domain-containing protein 154 OS=Homo sapiens GN=CCDC154 PE=2 SV=4 - [CC154_HUMAN]
Q9P0B6	Coiled-coil domain-containing protein 167 OS=Homo sapiens GN=CCDC167 PE=1 SV=2 - [CC167_HUMAN]
Q8NDH2	Coiled-coil domain-containing protein 168 OS=Homo sapiens GN=CCDC168 PE=2 SV=2 - [CC168_HUMAN]
Q9P1Z9	Coiled-coil domain-containing protein 180 OS=Homo sapiens GN=CCDC180 PE=2 SV=2 - [CC180_HUMAN]
Q5VVM6	Coiled-coil domain-containing protein 30 OS=Homo sapiens GN=CCDC30 PE=2 SV=1 - [CCD30_HUMAN]

Q8IWA6	Coiled-coil domain-containing protein 60 OS=Homo sapiens GN=CCDC60 PE=1 SV=2 - [CCD60_HUMAN]
Q8NA47	Coiled-coil domain-containing protein 63 OS=Homo sapiens GN=CCDC63 PE=2 SV=1 - [CCD63_HUMAN]
Q8IXS2	Coiled-coil domain-containing protein 65 OS=Homo sapiens GN=CCDC65 PE=1 SV=2 - [CCD65_HUMAN]
Q8IV32	Coiled-coil domain-containing protein 71 OS=Homo sapiens GN=CCDC71 PE=2 SV=3 - [CCD71_HUMAN]
Q6ZRK6	Coiled-coil domain-containing protein 73 OS=Homo sapiens GN=CCDC73 PE=2 SV=2 - [CCD73_HUMAN]
Q96AQ1	Coiled-coil domain-containing protein 74A OS=Homo sapiens GN=CCDC74A PE=2 SV=1 - [CC74A_HUMAN]
Q76M96	Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1 - [CCD80_HUMAN]
Q8N4S0	Coiled-coil domain-containing protein 82 OS=Homo sapiens GN=CCDC82 PE=1 SV=2 - [CCD82_HUMAN]
A6NC98	Coiled-coil domain-containing protein 88B OS=Homo sapiens GN=CCDC88B PE=1 SV=1 - [CC88B_HUMAN]
Q567U6	Coiled-coil domain-containing protein 93 OS=Homo sapiens GN=CCDC93 PE=1 SV=2 - [CCD93_HUMAN]
A1A4V9	Coiled-coil domain-containing protein C16orf93 OS=Homo sapiens GN=C16orf93 PE=2 SV=1 - [CP093_HUMAN]
Q8NCU4	Coiled-coil domain-containing protein KIAA1407 OS=Homo sapiens GN=KIAA1407 PE=2 SV=1 - [K1407_HUMAN]
Q9Y534	Cold shock domain-containing protein C2 OS=Homo sapiens GN=CSDC2 PE=1 SV=1 - [CSDC2_HUMAN]
P02452	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5 - [CO1A1_HUMAN]
P20908	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3 - [CO5A1_HUMAN]
Q02388	Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2 - [CO7A1_HUMAN]
Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]
Q5TAT6	Collagen alpha-1(XIII) chain OS=Homo sapiens GN=COL13A1 PE=1 SV=1 - [CODA1_HUMAN]
Q17RW2	Collagen alpha-1(XXIV) chain OS=Homo sapiens GN=COL24A1 PE=1 SV=2 - [COOA1_HUMAN]
Q9BXS0	Collagen alpha-1(XXV) chain OS=Homo sapiens GN=COL25A1 PE=1 SV=2 - [COPA1_HUMAN]
P12110	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4 - [CO6A2_HUMAN]
P25940	Collagen alpha-3(V) chain OS=Homo sapiens GN=COL5A3 PE=1 SV=3 - [CO5A3_HUMAN]
P12111	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5 - [CO6A3_HUMAN]
P53420	Collagen alpha-4(IV) chain OS=Homo sapiens GN=COL4A4 PE=1 SV=3 - [CO4A4_HUMAN]
A8TX70	Collagen alpha-5(VI) chain OS=Homo sapiens GN=COL6A5 PE=1 SV=1 - [CO6A5_HUMAN]
Q9H0A8	COMM domain-containing protein 4 OS=Homo sapiens GN=COMMD4 PE=1 SV=1 - [COMD4_HUMAN]
Q9BXJ2	Complement C1q tumor necrosis factor-related protein 7 OS=Homo sapiens GN=C1QTNF7 PE=2 SV=1 - [C1QT7_HUMAN]
P60827	Complement C1q tumor necrosis factor-related protein 8 OS=Homo sapiens GN=C1QTNF8 PE=1 SV=2 - [C1QT8_HUMAN]
P06681	Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2 - [CO2_HUMAN]
P07357	Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2 - [CO8A_HUMAN]
P08174	Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4 - [DAF_HUMAN]
P20023	Complement receptor type 2 OS=Homo sapiens GN=CR2 PE=1 SV=2 - [CR2_HUMAN]
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1 - [CND3_HUMAN]
P83436	Conserved oligomeric Golgi complex subunit 7 OS=Homo sapiens GN=COG7 PE=1 SV=1 - [COG7_HUMAN]
Q96MW5	Conserved oligomeric Golgi complex subunit 8 OS=Homo sapiens GN=COG8 PE=1 SV=2 - [COG8_HUMAN]
O94779	Contactin-5 OS=Homo sapiens GN=CNTN5 PE=1 SV=2 - [CNTN5_HUMAN]
Q9C0A0	Contactin-associated protein-like 4 OS=Homo sapiens GN=CNTNAP4 PE=1 SV=3 - [CNTP4_HUMAN]
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]
Q96A23	Copine-4 OS=Homo sapiens GN=CPNE4 PE=2 SV=1 - [CPNE4_HUMAN]
Q9UBL6	Copine-7 OS=Homo sapiens GN=CPNE7 PE=1 SV=1 - [CPNE7_HUMAN]
Q53SF7	Cordon-bleu protein-like 1 OS=Homo sapiens GN=COBLL1 PE=1 SV=2 - [COBL1_HUMAN]
P57737	Coronin-7 OS=Homo sapiens GN=CORO7 PE=1 SV=2 - [CORO7_HUMAN]
Q7Z7K0	COX assembly mitochondrial protein homolog OS=Homo sapiens GN=CMC1 PE=1 SV=1 - [COXM1_HUMAN]
Q8N123	CPX chromosomal region candidate gene 1 protein OS=Homo sapiens GN=CPXCR1 PE=2 SV=2 - [CPXCR_HUMAN]
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]
Q8IUR6	CREB3 regulatory factor OS=Homo sapiens GN=CREBRF PE=1 SV=2 - [CRERF_HUMAN]
Q5T3F8	CSC1-like protein 2 OS=Homo sapiens GN=TMEM63B PE=1 SV=1 - [CSCL2_HUMAN]
P56545	C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1 - [CTBP2_HUMAN]
Q9P126	C-type lectin domain family 1 member B OS=Homo sapiens GN=CLEC1B PE=1 SV=2 - [CLC1B_HUMAN]
Q8N1N0	C-type lectin domain family 4 member F OS=Homo sapiens GN=CLEC4F PE=2 SV=2 - [CLC4F_HUMAN]

Q9NY25	C-type lectin domain family 5 member A OS=Homo sapiens GN=CLEC5A PE=1 SV=1 - [CLC5A_HUMAN]
Q6EIG7	C-type lectin domain family 6 member A OS=Homo sapiens GN=CLEC6A PE=2 SV=1 - [CLC6A_HUMAN]
Q7Z408	CUB and sushi domain-containing protein 2 OS=Homo sapiens GN=CSMD2 PE=1 SV=2 - [CSMD2_HUMAN]
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]
Q13619	Cullin-4A OS=Homo sapiens GN=CUL4A PE=1 SV=3 - [CUL4A_HUMAN]
Q2TBE0	CWF19-like protein 2 OS=Homo sapiens GN=CWF19L2 PE=1 SV=4 - [C19L2_HUMAN]
Q9P0U4	CXXC-type zinc finger protein 1 OS=Homo sapiens GN=CXXC1 PE=1 SV=2 - [CXXC1_HUMAN]
Q8N884	Cyclic GMP-AMP synthase OS=Homo sapiens GN=MB21D1 PE=1 SV=2 - [CGAS_HUMAN]
P24863	Cyclin-C OS=Homo sapiens GN=CCNC PE=1 SV=2 - [CCNC_HUMAN]
Q14004	Cyclin-dependent kinase 13 OS=Homo sapiens GN=CDK13 PE=1 SV=2 - [CDK13_HUMAN]
Q07002	Cyclin-dependent kinase 18 OS=Homo sapiens GN=CDK18 PE=1 SV=3 - [CDK18_HUMAN]
P38936	Cyclin-dependent kinase inhibitor 1 OS=Homo sapiens GN=CDKN1A PE=1 SV=3 - [CDN1A_HUMAN]
O76039	Cyclin-dependent kinase-like 5 OS=Homo sapiens GN=CDKL5 PE=1 SV=1 - [CDKL5_HUMAN]
O14976	Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2 - [GAK_HUMAN]
Q8ND76	Cyclin-Y OS=Homo sapiens GN=CCNY PE=1 SV=2 - [CCNY_HUMAN]
Q14093	Cylicin-2 OS=Homo sapiens GN=CYLC2 PE=2 SV=1 - [CYLC2_HUMAN]
Q9NZV1	Cysteine-rich motor neuron 1 protein OS=Homo sapiens GN=CRIM1 PE=1 SV=1 - [CRIM1_HUMAN]
P54108	Cysteine-rich secretory protein 3 OS=Homo sapiens GN=CRISP3 PE=1 SV=1 - [CRIS3_HUMAN]
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]
P24310	Cytochrome c oxidase subunit 7A1, mitochondrial OS=Homo sapiens GN=COX7A1 PE=1 SV=2 - [CX7A1_HUMAN]
P53701	Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 - [CCHL_HUMAN]
O43174	Cytochrome P450 26A1 OS=Homo sapiens GN=CYP26A1 PE=2 SV=2 - [CP26A_HUMAN]
P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]
P98187	Cytochrome P450 4F8 OS=Homo sapiens GN=CYP4F8 PE=1 SV=1 - [CP4F8_HUMAN]
Q86W10	Cytochrome P450 4Z1 OS=Homo sapiens GN=CYP4Z1 PE=2 SV=1 - [CP4Z1_HUMAN]
Q8WWM9	Cytoglobin OS=Homo sapiens GN=CYGB PE=1 SV=1 - [CYGB_HUMAN]
Q15438	Cytohesin-1 OS=Homo sapiens GN=CYTH1 PE=1 SV=1 - [CYH1_HUMAN]
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]
Q8NCM8	Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4 - [DYHC2_HUMAN]
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]
O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]
Q96P26	Cytosolic 5'-nucleotidase 1B OS=Homo sapiens GN=NT5C1B PE=2 SV=2 - [5NT1B_HUMAN]
Q9UPW5	Cytosolic carboxypeptidase 1 OS=Homo sapiens GN=AGTPBP1 PE=1 SV=3 - [CBPC1_HUMAN]
P0C869	Cytosolic phospholipase A2 beta OS=Homo sapiens GN=PLA2G4B PE=1 SV=2 - [PA24B_HUMAN]
Q68DD2	Cytosolic phospholipase A2 zeta OS=Homo sapiens GN=PLA2G4F PE=2 SV=3 - [PA24F_HUMAN]
Q5M775	Cytospin-B OS=Homo sapiens GN=SPECC1 PE=1 SV=1 - [CYTSB_HUMAN]
P21918	D(1B) dopamine receptor OS=Homo sapiens GN=DRD5 PE=1 SV=2 - [DRD5_HUMAN]
Q8N465	D-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=D2HGDH PE=1 SV=3 - [D2HDH_HUMAN]
Q9HCK1	DBF4-type zinc finger-containing protein 2 OS=Homo sapiens GN=ZDBF2 PE=1 SV=3 - [ZDBF2_HUMAN]
Q8WV16	DDB1- and CUL4-associated factor 4 OS=Homo sapiens GN=DCAF4 PE=1 SV=3 - [DCAF4_HUMAN]
Q9UER7	Death domain-associated protein 6 OS=Homo sapiens GN=DAXX PE=1 SV=2 - [DAXX_HUMAN]
Q6ZMT9	Death domain-containing protein 1 OS=Homo sapiens GN=DTHD1 PE=2 SV=3 - [DTHD1_HUMAN]
P53355	Death-associated protein kinase 1 OS=Homo sapiens GN=DAPK1 PE=1 SV=6 - [DAPK1_HUMAN]
O43293	Death-associated protein kinase 3 OS=Homo sapiens GN=DAPK3 PE=1 SV=1 - [DAPK3_HUMAN]
Q96BY6	Dedicator of cytokinesis protein 10 OS=Homo sapiens GN=DOCK10 PE=1 SV=3 - [DOC10_HUMAN]
Q5JSL3	Dedicator of cytokinesis protein 11 OS=Homo sapiens GN=DOCK11 PE=1 SV=2 - [DOC11_HUMAN]
Q8IZD9	Dedicator of cytokinesis protein 3 OS=Homo sapiens GN=DOCK3 PE=1 SV=1 - [DOCK3_HUMAN]
Q96HP0	Dedicator of cytokinesis protein 6 OS=Homo sapiens GN=DOCK6 PE=1 SV=3 - [DOCK6_HUMAN]
Q8NF50	Dedicator of cytokinesis protein 8 OS=Homo sapiens GN=DOCK8 PE=1 SV=3 - [DOCK8_HUMAN]
Q9BZ29	Dedicator of cytokinesis protein 9 OS=Homo sapiens GN=DOCK9 PE=1 SV=2 - [DOCK9_HUMAN]

Q9Y238	Deleted in lung and esophageal cancer protein 1 OS=Homo sapiens GN=DLEC1 PE=2 SV=2 - [DLEC1_HUMAN]
Q9NR61	Delta-like protein 4 OS=Homo sapiens GN=DLL4 PE=1 SV=1 - [DLL4_HUMAN]
Q08495	Dematin OS=Homo sapiens GN=DMTN PE=1 SV=3 - [DEMA_HUMAN]
Q8TEH3	DENN domain-containing protein 1A OS=Homo sapiens GN=DENND1A PE=1 SV=2 - [DEN1A_HUMAN]
Q6IQ26	DENN domain-containing protein 5A OS=Homo sapiens GN=DENND5A PE=1 SV=2 - [DEN5A_HUMAN]
Q16854	Deoxyguanosine kinase, mitochondrial OS=Homo sapiens GN=DGUOK PE=1 SV=2 - [DGUOK_HUMAN]
Q9H147	Deoxynucleotidyltransferase terminal-interacting protein 1 OS=Homo sapiens GN=DNTTIP1 PE=1 SV=2 - [TDIF1_HUMAN]
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]
P17661	Desmin OS=Homo sapiens GN=DES PE=1 SV=3 - [DESM_HUMAN]
Q02487	Desmocollin-2 OS=Homo sapiens GN=DSC2 PE=1 SV=1 - [DSC2_HUMAN]
Q14574	Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3 - [DSC3_HUMAN]
Q02413	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 - [DSG1_HUMAN]
Q16760	Diacylglycerol kinase delta OS=Homo sapiens GN=DGKD PE=1 SV=4 - [DGKD_HUMAN]
P49619	Diacylglycerol kinase gamma OS=Homo sapiens GN=DGKG PE=2 SV=3 - [DGKG_HUMAN]
P52824	Diacylglycerol kinase theta OS=Homo sapiens GN=DGKQ PE=1 SV=2 - [DGKQ_HUMAN]
Q9UBU2	Dickkopf-related protein 2 OS=Homo sapiens GN=DKK2 PE=2 SV=1 - [DKK2_HUMAN]
Q3MIW9	Diffuse panbronchiolitis critical region protein 1 OS=Homo sapiens GN=DPCR1 PE=2 SV=2 - [DPCR1_HUMAN]
Q9BQC3	Diphthamide biosynthesis protein 2 OS=Homo sapiens GN=DPH2 PE=1 SV=1 - [DPH2_HUMAN]
Q8TF46	DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DI3L1_HUMAN]
Q16832	Discoidin domain-containing receptor 2 OS=Homo sapiens GN=DDR2 PE=1 SV=2 - [DDR2_HUMAN]
Q14689	Disco-interacting protein 2 homolog A OS=Homo sapiens GN=DIP2A PE=1 SV=2 - [DIP2A_HUMAN]
Q86T65	Disheveled-associated activator of morphogenesis 2 OS=Homo sapiens GN=DAAM2 PE=1 SV=3 - [DAAM2_HUMAN]
P78536	Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1 - [ADA17_HUMAN]
Q9Y3Q7	Disintegrin and metalloproteinase domain-containing protein 18 OS=Homo sapiens GN=ADAM18 PE=2 SV=1 - [ADA18_HUMAN]
Q9UKQ2	Disintegrin and metalloproteinase domain-containing protein 28 OS=Homo sapiens GN=ADAM28 PE=2 SV=3 - [ADA28_HUMAN]
Q8TDM6	Disks large homolog 5 OS=Homo sapiens GN=DLG5 PE=1 SV=4 - [DLG5_HUMAN]
O95886	Disks large-associated protein 3 OS=Homo sapiens GN=DLGAP3 PE=1 SV=3 - [DLGP3_HUMAN]
Q9Y485	DmX-like protein 1 OS=Homo sapiens GN=DMXL1 PE=1 SV=3 - [DMXL1_HUMAN]
Q8TDJ6	DmX-like protein 2 OS=Homo sapiens GN=DMXL2 PE=1 SV=2 - [DMXL2_HUMAN]
Q9Y6K1	DNA (cytosine-5)-methyltransferase 3A OS=Homo sapiens GN=DNMT3A PE=1 SV=4 - [DNM3A_HUMAN]
Q9UBC3	DNA (cytosine-5)-methyltransferase 3B OS=Homo sapiens GN=DNMT3B PE=1 SV=1 - [DNM3B_HUMAN]
Q6PJP8	DNA cross-link repair 1A protein OS=Homo sapiens GN=DCLRE1A PE=1 SV=3 - [DCR1A_HUMAN]
Q96D03	DNA damage-inducible transcript 4-like protein OS=Homo sapiens GN=DDIT4L PE=1 SV=1 - [DDT4L_HUMAN]
Q9ULG1	DNA helicase INO80 OS=Homo sapiens GN=INO80 PE=1 SV=2 - [INO80_HUMAN]
Q9NPF5	DNA methyltransferase 1-associated protein 1 OS=Homo sapiens GN=DMAP1 PE=1 SV=1 - [DMAP1_HUMAN]
P40692	DNA mismatch repair protein Mlh1 OS=Homo sapiens GN=MLH1 PE=1 SV=1 - [MLH1_HUMAN]
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1 - [MSH2_HUMAN]
Q15054	DNA polymerase delta subunit 3 OS=Homo sapiens GN=POLD3 PE=1 SV=2 - [DPOD3_HUMAN]
Q07864	DNA polymerase epsilon catalytic subunit A OS=Homo sapiens GN=POLE PE=1 SV=5 - [DPOE1_HUMAN]
Q9Y253	DNA polymerase eta OS=Homo sapiens GN=POLH PE=1 SV=1 - [POLH_HUMAN]
Q9UBT6	DNA polymerase kappa OS=Homo sapiens GN=POLK PE=1 SV=1 - [POLK_HUMAN]
P54098	DNA polymerase subunit gamma-1 OS=Homo sapiens GN=POLG PE=1 SV=1 - [DPOG1_HUMAN]
O75417	DNA polymerase theta OS=Homo sapiens GN=POLQ PE=1 SV=2 - [DPOLQ_HUMAN]
O60673	DNA polymerase zeta catalytic subunit OS=Homo sapiens GN=REV3L PE=1 SV=2 - [DPOLZ_HUMAN]
Q92698	DNA repair and recombination protein RAD54-like OS=Homo sapiens GN=RAD54L PE=1 SV=2 - [RAD54_HUMAN]
P23025	DNA repair protein complementing XP-A cells OS=Homo sapiens GN=XPA PE=1 SV=1 - [XPA_HUMAN]
Q01831	DNA repair protein complementing XP-C cells OS=Homo sapiens GN=XPC PE=1 SV=4 - [XPC_HUMAN]
Q92878	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1 - [RAD50_HUMAN]

Q9UBZ9	DNA repair protein REV1 OS=Homo sapiens GN=REV1 PE=1 SV=1 - [REV1_HUMAN]
P51530	DNA replication ATP-dependent helicase/nuclease DNA2 OS=Homo sapiens GN=DNA2 PE=1 SV=3 - [DNA2_HUMAN]
P33991	DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN]
P33992	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 - [MCM5_HUMAN]
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]
Q02880	DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3 - [TOP2B_HUMAN]
Q9H5L6	DNA transposase THAP9 OS=Homo sapiens GN=THAP9 PE=1 SV=2 - [THAP9_HUMAN]
Q2KHR2	DNA-binding protein RFX7 OS=Homo sapiens GN=RFX7 PE=1 SV=1 - [RFX7_HUMAN]
Q01826	DNA-binding protein SATB1 OS=Homo sapiens GN=SATB1 PE=1 SV=1 - [SATB1_HUMAN]
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]
Q9NP87	DNA-directed DNA/RNA polymerase mu OS=Homo sapiens GN=POLM PE=1 SV=1 - [DPOLM_HUMAN]
O95602	DNA-directed RNA polymerase I subunit RPA1 OS=Homo sapiens GN=POLR1A PE=1 SV=2 - [RPA1_HUMAN]
O14802	DNA-directed RNA polymerase III subunit RPC1 OS=Homo sapiens GN=POLR3A PE=1 SV=2 - [RPC1_HUMAN]
O00411	DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2 - [RPOM_HUMAN]
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Homo sapiens GN=POLR2E PE=1 SV=4 - [RPAB1_HUMAN]
P59910	DnaJ homolog subfamily B member 13 OS=Homo sapiens GN=DNAJB13 PE=2 SV=1 - [DJB13_HUMAN]
Q9NVH1	DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2 - [DJC11_HUMAN]
Q9NNZ3	DnaJ homolog subfamily C member 4 OS=Homo sapiens GN=DNAJC4 PE=1 SV=1 - [DNJC4_HUMAN]
O60496	Docking protein 2 OS=Homo sapiens GN=DOK2 PE=1 SV=2 - [DOK2_HUMAN]
Q6PKX4	Docking protein 6 OS=Homo sapiens GN=DOK6 PE=1 SV=1 - [DOK6_HUMAN]
O60762	Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens GN=DPM1 PE=1 SV=1 - [DPM1_HUMAN]
Q9Y672	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase OS=Homo sapiens GN=ALG6 PE=1 SV=1 - [ALG6_HUMAN]
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2 - [STT3A_HUMAN]
Q92685	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase OS=Homo sapiens GN=ALG3 PE=1 SV=1 - [ALG3_HUMAN]
Q6RFH8	Double homeobox protein 4C OS=Homo sapiens GN=DUX4L9 PE=1 SV=1 - [DUX4C_HUMAN]
P49959	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3 - [MRE11_HUMAN]
Q9NUL3	Double-stranded RNA-binding protein Staufen homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1 - [STAU2_HUMAN]
O60469	Down syndrome cell adhesion molecule OS=Homo sapiens GN=DSCAM PE=1 SV=2 - [DSCAM_HUMAN]
Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]
P45985	Dual specificity mitogen-activated protein kinase kinase 4 OS=Homo sapiens GN=MAP2K4 PE=1 SV=1 - [MP2K4_HUMAN]
Q13163	Dual specificity mitogen-activated protein kinase kinase 5 OS=Homo sapiens GN=MAP2K5 PE=1 SV=2 - [MP2K5_HUMAN]
O14733	Dual specificity mitogen-activated protein kinase kinase 7 OS=Homo sapiens GN=MAP2K7 PE=1 SV=2 - [MP2K7_HUMAN]
Q9Y6W6	Dual specificity protein phosphatase 10 OS=Homo sapiens GN=DUSP10 PE=1 SV=1 - [DUS10_HUMAN]
Q6B8I1	Dual specificity protein phosphatase 13 isoform A OS=Homo sapiens GN=DUSP13 PE=1 SV=1 - [DS13A_HUMAN]
Q9UII6	Dual specificity protein phosphatase 13 isoform B OS=Homo sapiens GN=DUSP13 PE=1 SV=3 - [DS13B_HUMAN]
Q9H596	Dual specificity protein phosphatase 21 OS=Homo sapiens GN=DUSP21 PE=1 SV=1 - [DUS21_HUMAN]
Q9UNH5	Dual specificity protein phosphatase CDC14A OS=Homo sapiens GN=CDC14A PE=1 SV=1 - [CC14A_HUMAN]
Q96S53	Dual specificity testis-specific protein kinase 2 OS=Homo sapiens GN=TESK2 PE=1 SV=1 - [TESK2_HUMAN]
Q6XZF7	Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=1 SV=1 - [DNMBP_HUMAN]
O60313	Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3 - [OPA1_HUMAN]
Q8IVF4	Dynein heavy chain 10, axonemal OS=Homo sapiens GN=DNAH10 PE=1 SV=4 - [DYH10_HUMAN]
Q96DT5	Dynein heavy chain 11, axonemal OS=Homo sapiens GN=DNAH11 PE=1 SV=4 - [DYH11_HUMAN]
Q9UFH2	Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=1 SV=2 - [DYH17_HUMAN]

Q8TD57	Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1 - [DYH3_HUMAN]
Q8TE73	Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]
Q8WXX0	Dynein heavy chain 7, axonemal OS=Homo sapiens GN=DNAH7 PE=1 SV=2 - [DYH7_HUMAN]
Q9NYC9	Dynein heavy chain 9, axonemal OS=Homo sapiens GN=DNAH9 PE=1 SV=3 - [DYH9_HUMAN]
Q96M86	Dynein heavy chain domain-containing protein 1 OS=Homo sapiens GN=DNHD1 PE=2 SV=2 - [DNHD1_HUMAN]
Q5VV43	Dyslexia-associated protein KIAA0319 OS=Homo sapiens GN=KIAA0319 PE=1 SV=1 - [K0319_HUMAN]
Q03001	Dystonin OS=Homo sapiens GN=DST PE=1 SV=4 - [DYST_HUMAN]
P11532	Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3 - [DMD_HUMAN]
O00257	E3 SUMO-protein ligase CBX4 OS=Homo sapiens GN=CBX4 PE=1 SV=3 - [CBX4_HUMAN]
O75150	E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=4 - [BRE1B_HUMAN]
Q13191	E3 ubiquitin-protein ligase CBL-B OS=Homo sapiens GN=CBLB PE=1 SV=2 - [CBLB_HUMAN]
Q9UNE7	E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2 - [CHIP_HUMAN]
Q9Y2E6	E3 ubiquitin-protein ligase DTX4 OS=Homo sapiens GN=DTX4 PE=1 SV=2 - [DTX4_HUMAN]
Q9ULT8	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3 - [HECD1_HUMAN]
O95714	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 - [HERC2_HUMAN]
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]
O94822	E3 ubiquitin-protein ligase listerin OS=Homo sapiens GN=LTN1 PE=1 SV=6 - [LTN1_HUMAN]
Q8TBB1	E3 ubiquitin-protein ligase LNX OS=Homo sapiens GN=LNX1 PE=1 SV=1 - [LNX1_HUMAN]
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 OS=Homo sapiens GN=LRSAM1 PE=1 SV=1 - [LRSM1_HUMAN]
Q9UHC7	E3 ubiquitin-protein ligase makorin-1 OS=Homo sapiens GN=MKRN1 PE=1 SV=3 - [MKRN1_HUMAN]
O75592	E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=1 SV=3 - [MYCB2_HUMAN]
P46934	E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4 PE=1 SV=4 - [NEDD4_HUMAN]
Q8NG27	E3 ubiquitin-protein ligase Praja-1 OS=Homo sapiens GN=PJA1 PE=1 SV=2 - [PJA1_HUMAN]
Q7Z6E9	E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1 - [RBBP6_HUMAN]
Q86XS8	E3 ubiquitin-protein ligase RNF130 OS=Homo sapiens GN=RNF130 PE=1 SV=1 - [GOLI_HUMAN]
Q8NCN4	E3 ubiquitin-protein ligase RNF169 OS=Homo sapiens GN=RNF169 PE=1 SV=2 - [RN169_HUMAN]
Q63HN8	E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3 - [RN213_HUMAN]
Q96EP0	E3 ubiquitin-protein ligase RNF31 OS=Homo sapiens GN=RNF31 PE=1 SV=1 - [RNF31_HUMAN]
Q9Y252	E3 ubiquitin-protein ligase RNF6 OS=Homo sapiens GN=RNF6 PE=1 SV=1 - [RNF6_HUMAN]
Q9NS56	E3 ubiquitin-protein ligase Topors OS=Homo sapiens GN=TOPORS PE=1 SV=1 - [TOPRS_HUMAN]
Q9BZY9	E3 ubiquitin-protein ligase TRIM31 OS=Homo sapiens GN=TRIM31 PE=1 SV=2 - [TRI31_HUMAN]
Q13049	E3 ubiquitin-protein ligase TRIM32 OS=Homo sapiens GN=TRIM32 PE=1 SV=2 - [TRI32_HUMAN]
Q8WV44	E3 ubiquitin-protein ligase TRIM41 OS=Homo sapiens GN=TRIM41 PE=1 SV=3 - [TRI41_HUMAN]
Q9BRZ2	E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3 - [TRI56_HUMAN]
Q6AZZ1	E3 ubiquitin-protein ligase TRIM68 OS=Homo sapiens GN=TRIM68 PE=1 SV=1 - [TRI68_HUMAN]
Q14669	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 - [TRIPC_HUMAN]
Q8IWV7	E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens GN=UBR1 PE=1 SV=1 - [UBR1_HUMAN]
Q6ZT12	E3 ubiquitin-protein ligase UBR3 OS=Homo sapiens GN=UBR3 PE=2 SV=2 - [UBR3_HUMAN]
Q9HC35	Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3 - [EMAL4_HUMAN]
Q9Y5L3	Ectonucleoside triphosphate diphosphohydrolase 2 OS=Homo sapiens GN=ENTPD2 PE=1 SV=1 - [ENTP2_HUMAN]
Q9Y227	Ectonucleoside triphosphate diphosphohydrolase 4 OS=Homo sapiens GN=ENTPD4 PE=1 SV=1 - [ENTP4_HUMAN]
O14638	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Homo sapiens GN=ENPP3 PE=1 SV=2 - [ENPP3_HUMAN]
Q9HCE0	Ectopic P granules protein 5 homolog OS=Homo sapiens GN=EPG5 PE=2 SV=2 - [EPG5_HUMAN]
Q9HA90	EF-hand and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=EFCC1 PE=2 SV=2 - [EFCC1_HUMAN]
Q8IY85	EF-hand calcium-binding domain-containing protein 13 OS=Homo sapiens GN=EFCAB13 PE=2 SV=2 - [EFC13_HUMAN]
A4FU69	EF-hand calcium-binding domain-containing protein 5 OS=Homo sapiens GN=EFCAB5 PE=1 SV=3 - [EFCB5_HUMAN]
Q5JVL4	EF-hand domain-containing protein 1 OS=Homo sapiens GN=EFHC1 PE=1 SV=1 - [EFHC1_HUMAN]
Q8N3D4	EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHBP1L1 PE=1 SV=2 - [EH1L1_HUMAN]
Q9BY07	Electrogenic sodium bicarbonate cotransporter 4 OS=Homo sapiens GN=SLC4A5 PE=2 SV=2 - [S4A5_HUMAN]

P57679	Ellis-van Creveld syndrome protein OS=Homo sapiens GN=EVC PE=1 SV=1 - [EVC_HUMAN]
Q6PJG2	ELM2 and SANT domain-containing protein 1 OS=Homo sapiens GN=ELMSAN1 PE=1 SV=2 - [EMSA1_HUMAN]
Q96FG2	ELMO domain-containing protein 3 OS=Homo sapiens GN=ELMOD3 PE=1 SV=2 - [ELMD3_HUMAN]
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]
Q9Y6C2	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2 - [EMIL1_HUMAN]
Q9YNA8	Endogenous retrovirus group K member 19 Gag polyprotein OS=Homo sapiens GN=ERVK-19 PE=1 SV=3 - [GAK19_HUMAN]
P61566	Endogenous retrovirus group K member 24 Env polyprotein OS=Homo sapiens GN=ERVK-24 PE=2 SV=1 - [ENK24_HUMAN]
Q7LDI9	Endogenous retrovirus group K member 6 Gag polyprotein OS=Homo sapiens GN=ERVK-6 PE=1 SV=3 - [GAK6_HUMAN]
P63135	Endogenous retrovirus group K member 7 Pol protein OS=Homo sapiens GN=ERVK-7 PE=3 SV=1 - [POK7_HUMAN]
Q9UKH3	Endogenous retrovirus group K member 9 Env polyprotein OS=Homo sapiens GN=ERVK-9 PE=1 SV=1 - [ENK9_HUMAN]
P61550	Endogenous retrovirus group S71 member 1 Env polyprotein OS=Homo sapiens GN=ERVS71-1 PE=2 SV=1 - [ENVT1_HUMAN]
Q96FI4	Endonuclease 8-like 1 OS=Homo sapiens GN=NEIL1 PE=1 SV=3 - [NEIL1_HUMAN]
Q14249	Endonuclease G, mitochondrial OS=Homo sapiens GN=ENDOG PE=1 SV=4 - [NUCG_HUMAN]
Q99961	Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 - [SH3G1_HUMAN]
Q6P179	Endoplasmic reticulum aminopeptidase 2 OS=Homo sapiens GN=ERAP2 PE=1 SV=2 - [ERAP2_HUMAN]
Q9UPY3	Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3 - [DICER_HUMAN]
P24530	Endothelin B receptor OS=Homo sapiens GN=EDNRB PE=1 SV=1 - [EDNRB_HUMAN]
P42892	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2 - [ECE1_HUMAN]
Q96JJ3	Engulfment and cell motility protein 2 OS=Homo sapiens GN=ELMO2 PE=1 SV=2 - [ELMO2_HUMAN]
Q96BJ8	Engulfment and cell motility protein 3 OS=Homo sapiens GN=ELMO3 PE=2 SV=3 - [ELMO3_HUMAN]
Q6P2E9	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1 - [EDC4_HUMAN]
P42126	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1 - [ECI1_HUMAN]
Q96DC8	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Homo sapiens GN=ECHDC3 PE=1 SV=2 - [ECHD3_HUMAN]
Q92817	Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3 - [EVPL_HUMAN]
P12724	Eosinophil cationic protein OS=Homo sapiens GN=RNASE3 PE=1 SV=2 - [ECP_HUMAN]
P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]
P29323	Ephrin type-B receptor 2 OS=Homo sapiens GN=EPHB2 PE=1 SV=5 - [EPHB2_HUMAN]
P20827	Ephrin-A1 OS=Homo sapiens GN=EFNA1 PE=1 SV=2 - [EFNA1_HUMAN]
Q8TE67	Epidermal growth factor receptor kinase substrate 8-like protein 3 OS=Homo sapiens GN=EPS8L3 PE=1 SV=2 - [ES8L3_HUMAN]
Q9UHF1	Epidermal growth factor-like protein 7 OS=Homo sapiens GN=EGFL7 PE=1 SV=3 - [EGFL7_HUMAN]
Q99645	Epiphycan OS=Homo sapiens GN=EPYC PE=2 SV=3 - [EPYC_HUMAN]
P58107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]
Q6NXG1	Epithelial splicing regulatory protein 1 OS=Homo sapiens GN=ESRP1 PE=1 SV=2 - [ESRP1_HUMAN]
O95925	Eppin OS=Homo sapiens GN=EPPIN PE=1 SV=1 - [EPPI_HUMAN]
Q9BV94	ER degradation-enhancing alpha-mannosidase-like protein 2 OS=Homo sapiens GN=EDEM2 PE=1 SV=2 - [EDEM2_HUMAN]
Q8N766	ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1 - [EMC1_HUMAN]
Q5UCC4	ER membrane protein complex subunit 10 OS=Homo sapiens GN=EMC10 PE=1 SV=1 - [EMC10_HUMAN]
Q9H501	ESF1 homolog OS=Homo sapiens GN=ESF1 PE=1 SV=1 - [ESF1_HUMAN]
Q6ZN32	ETS translocation variant 3-like protein OS=Homo sapiens GN=ETV3L PE=2 SV=1 - [ETV3L_HUMAN]
O00418	Eukaryotic elongation factor 2 kinase OS=Homo sapiens GN=EEF2K PE=1 SV=2 - [EF2K_HUMAN]
P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [ERF3A_HUMAN]
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3 - [ERF1_HUMAN]
Q9NZJ5	Eukaryotic translation initiation factor 2-alpha kinase 3 OS=Homo sapiens GN=EIF2AK3 PE=1 SV=3 - [E2AK3_HUMAN]
P41214	Eukaryotic translation initiation factor 2D OS=Homo sapiens GN=EIF2D PE=1 SV=3 - [EIF2D_HUMAN]
O75822	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2 - [EIF3J_HUMAN]
Q04637	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 - [IF4G1_HUMAN]

P78344	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1 - [IF4G2_HUMAN]
Q9NRA8	Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 PE=1 SV=2 - [4ET_HUMAN]
Q15056	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 - [IF4H_HUMAN]
Q9GZV4	Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3 - [IF5A2_HUMAN]
P43004	Excitatory amino acid transporter 2 OS=Homo sapiens GN=SLC1A2 PE=1 SV=2 - [EAA2_HUMAN]
O00471	Exocyst complex component 5 OS=Homo sapiens GN=EXOC5 PE=1 SV=1 - [EXOC5_HUMAN]
Q9UQ84	Exonuclease 1 OS=Homo sapiens GN=EXO1 PE=1 SV=2 - [EXO1_HUMAN]
Q9NVH0	Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2 - [EXD2_HUMAN]
Q8NEV8	Exophilin-5 OS=Homo sapiens GN=EXPH5 PE=1 SV=3 - [EXPH5_HUMAN]
Q9NQT4	Exosome complex component RRP46 OS=Homo sapiens GN=EXOSC5 PE=1 SV=1 - [EXOS5_HUMAN]
Q01780	Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 - [EXOSX_HUMAN]
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]
Q96QU8	Exportin-6 OS=Homo sapiens GN=XPO6 PE=1 SV=1 - [XPO6_HUMAN]
A0FGR9	Extended synaptotagmin-3 OS=Homo sapiens GN=ESYT3 PE=1 SV=1 - [ESYT3_HUMAN]
P41180	Extracellular calcium-sensing receptor OS=Homo sapiens GN=CASR PE=1 SV=2 - [CASR_HUMAN]
Q86XX4	Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 PE=1 SV=2 - [FRAS1_HUMAN]
Q8IWU6	Extracellular sulfatase Sulf-1 OS=Homo sapiens GN=SULF1 PE=1 SV=1 - [SULF1_HUMAN]
Q6QHK4	Factor in the germline alpha OS=Homo sapiens GN=FIGLA PE=1 SV=2 - [FIGLA_HUMAN]
Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=1 SV=2 - [FXRD1_HUMAN]
O15360	Fanconi anemia group A protein OS=Homo sapiens GN=FANCA PE=1 SV=2 - [FANCA_HUMAN]
Q9BXW9	Fanconi anemia group D2 protein OS=Homo sapiens GN=FANCD2 PE=1 SV=2 - [FACD2_HUMAN]
Q8IYD8	Fanconi anemia group M protein OS=Homo sapiens GN=FANCM PE=1 SV=2 - [FANCM_HUMAN]
Q53R41	FAST kinase domain-containing protein 1 OS=Homo sapiens GN=FASTKD1 PE=1 SV=1 - [FAKD1_HUMAN]
Q14CZ7	FAST kinase domain-containing protein 3 OS=Homo sapiens GN=FASTKD3 PE=1 SV=2 - [FAKD3_HUMAN]
Q8NCQ5	F-box only protein 15 OS=Homo sapiens GN=FBXO15 PE=2 SV=2 - [FBX15_HUMAN]
Q6PIJ6	F-box only protein 38 OS=Homo sapiens GN=FBXO38 PE=1 SV=3 - [FBX38_HUMAN]
Q9NRD1	F-box only protein 6 OS=Homo sapiens GN=FBXO6 PE=1 SV=1 - [FBX6_HUMAN]
Q8N1E6	F-box/LRR-repeat protein 14 OS=Homo sapiens GN=FBXL14 PE=1 SV=1 - [FXL14_HUMAN]
Q9UJT9	F-box/LRR-repeat protein 7 OS=Homo sapiens GN=FBXL7 PE=2 SV=1 - [FBXL7_HUMAN]
Q9Y297	F-box/WD repeat-containing protein 1A OS=Homo sapiens GN=BTRC PE=1 SV=1 - [FBW1A_HUMAN]
Q96RD9	Fc receptor-like protein 5 OS=Homo sapiens GN=FCRL5 PE=1 SV=3 - [FCRL5_HUMAN]
A0AVI2	Fer-1-like protein 5 OS=Homo sapiens GN=FER1L5 PE=2 SV=2 - [FR1L5_HUMAN]
Q2WGJ9	Fer-1-like protein 6 OS=Homo sapiens GN=FER1L6 PE=2 SV=2 - [FR1L6_HUMAN]
Q68DX3	FERM and PDZ domain-containing protein 2 OS=Homo sapiens GN=FRMPD2 PE=1 SV=3 - [FRPD2_HUMAN]
Q5JV73	FERM and PDZ domain-containing protein 3 OS=Homo sapiens GN=FRMPD3 PE=2 SV=2 - [FRPD3_HUMAN]
Q14CM0	FERM and PDZ domain-containing protein 4 OS=Homo sapiens GN=FRMPD4 PE=1 SV=1 - [FRPD4_HUMAN]
Q8N878	FERM domain-containing protein 1 OS=Homo sapiens GN=FRMD1 PE=2 SV=2 - [FRMD1_HUMAN]
Q9Y2L6	FERM domain-containing protein 4B OS=Homo sapiens GN=FRMD4B PE=1 SV=4 - [FRM4B_HUMAN]
Q9Y4F1	FERM, RhoGEF and pleckstrin domain-containing protein 1 OS=Homo sapiens GN=FARP1 PE=1 SV=1 - [FARP1_HUMAN]
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 - [FRIL_HUMAN]
Q969F0	Fetal and adult testis-expressed transcript protein OS=Homo sapiens GN=FATE1 PE=1 SV=1 - [FATE1_HUMAN]
A0PJY2	Fez family zinc finger protein 1 OS=Homo sapiens GN=FEZF1 PE=1 SV=1 - [FEZF1_HUMAN]
P35555	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMAN]
P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2 - [FIBB_HUMAN]
P09038	Fibroblast growth factor 2 OS=Homo sapiens GN=FGF2 PE=1 SV=3 - [FGF2_HUMAN]
P08620	Fibroblast growth factor 4 OS=Homo sapiens GN=FGF4 PE=1 SV=1 - [FGF4_HUMAN]
Q86WI1	Fibrocystin-L OS=Homo sapiens GN=PKHD1L1 PE=2 SV=2 - [PKHL1_HUMAN]
Q4ZHG4	Fibronectin type III domain-containing protein 1 OS=Homo sapiens GN=FNDC1 PE=2 SV=4 - [FNDC1_HUMAN]
Q5CZC0	Fibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=2 SV=4 - [FSIP2_HUMAN]

P20930	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3 - [FILA_HUMAN]
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]
P39748	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN]
O75955	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 - [FLOT1_HUMAN]
Q4VC44	FLYWCH-type zinc finger-containing protein 1 OS=Homo sapiens GN=FLYWCH1 PE=1 SV=2 - [FWCH1_HUMAN]
P41440	Folate transporter 1 OS=Homo sapiens GN=SLC19A1 PE=1 SV=3 - [S19A1_HUMAN]
P23945	Follicle-stimulating hormone receptor OS=Homo sapiens GN=FSHR PE=1 SV=3 - [FSHR_HUMAN]
Q9P278	Folliculin-interacting protein 2 OS=Homo sapiens GN=FNIP2 PE=1 SV=2 - [FNIP2_HUMAN]
P98177	Forkhead box protein O4 OS=Homo sapiens GN=FOXO4 PE=1 SV=5 - [FOXO4_HUMAN]
O43638	Forkhead box protein S1 OS=Homo sapiens GN=FOXS1 PE=2 SV=2 - [FOXS1_HUMAN]
Q9NZ56	Formin-2 OS=Homo sapiens GN=FMN2 PE=1 SV=4 - [FMN2_HUMAN]
Q8N3X1	Formin-binding protein 4 OS=Homo sapiens GN=FNBP4 PE=1 SV=3 - [FNBP4_HUMAN]
P15408	Fos-related antigen 2 OS=Homo sapiens GN=FOSL2 PE=1 SV=1 - [FOSL2_HUMAN]
P51114	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3 - [FXR1_HUMAN]
Q9UP38	Frizzled-1 OS=Homo sapiens GN=FZD1 PE=1 SV=2 - [FZD1_HUMAN]
Q9ULV1	Frizzled-4 OS=Homo sapiens GN=FZD4 PE=1 SV=2 - [FZD4_HUMAN]
Q13467	Frizzled-5 OS=Homo sapiens GN=FZD5 PE=1 SV=2 - [FZD5_HUMAN]
Q9H479	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1 - [FN3K_HUMAN]
P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]
O75072	Fukutin OS=Homo sapiens GN=FKTN PE=1 SV=2 - [FKTN_HUMAN]
Q6P2I3	Fumarylacetoacetate hydrolase domain-containing protein 2B OS=Homo sapiens GN=FAHD2B PE=2 SV=1 - [FAH2B_HUMAN]
O15117	FYN-binding protein OS=Homo sapiens GN=FYB PE=1 SV=2 - [FYB_HUMAN]
Q6ZV73	FYVE, RhoGEF and PH domain-containing protein 6 OS=Homo sapiens GN=FGD6 PE=1 SV=2 - [FGD6_HUMAN]
Q9UKJ3	G patch domain-containing protein 8 OS=Homo sapiens GN=GPATCH8 PE=1 SV=2 - [GPTC8_HUMAN]
P48549	G protein-activated inward rectifier potassium channel 1 OS=Homo sapiens GN=KCNJ3 PE=1 SV=1 - [KCNJ3_HUMAN]
Q92806	G protein-activated inward rectifier potassium channel 3 OS=Homo sapiens GN=KCNJ9 PE=2 SV=2 - [KCNJ9_HUMAN]
P27469	G0/G1 switch protein 2 OS=Homo sapiens GN=G0S2 PE=1 SV=1 - [G0S2_HUMAN]
Q9NYZ3	G2 and S phase-expressed protein 1 OS=Homo sapiens GN=GTSE1 PE=1 SV=3 - [GTSE1_HUMAN]
Q7L622	G2/M phase-specific E3 ubiquitin-protein ligase OS=Homo sapiens GN=G2E3 PE=1 SV=1 - [G2E3_HUMAN]
Q8WWL7	G2/mitotic-specific cyclin-B3 OS=Homo sapiens GN=CCNB3 PE=1 SV=2 - [CCNB3_HUMAN]
Q06546	GA-binding protein alpha chain OS=Homo sapiens GN=GABPA PE=1 SV=1 - [GABPA_HUMAN]
P07902	Galactose-1-phosphate uridylyltransferase OS=Homo sapiens GN=GALT PE=1 SV=3 - [GALT_HUMAN]
P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]
Q86UU5	Gametogenetin OS=Homo sapiens GN=GGN PE=1 SV=2 - [GGN_HUMAN]
P24046	Gamma-aminobutyric acid receptor subunit rho-1 OS=Homo sapiens GN=GABRR1 PE=2 SV=2 - [GBRR1_HUMAN]
Q9UBS5	Gamma-aminobutyric acid type B receptor subunit 1 OS=Homo sapiens GN=GABBR1 PE=1 SV=1 - [GABR1_HUMAN]
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]
Q9UJ14	Gamma-glutamyltransferase 7 OS=Homo sapiens GN=GGT7 PE=1 SV=2 - [GGT7_HUMAN]
Q9HBI0	Gamma-parvin OS=Homo sapiens GN=PARVG PE=1 SV=1 - [PARVG_HUMAN]
Q9BSJ2	Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=1 SV=2 - [GCP2_HUMAN]
P17302	Gap junction alpha-1 protein OS=Homo sapiens GN=GJA1 PE=1 SV=2 - [CXA1_HUMAN]
Q9Y6H8	Gap junction alpha-3 protein OS=Homo sapiens GN=GJA3 PE=1 SV=4 - [CXA3_HUMAN]
P57773	Gap junction alpha-9 protein OS=Homo sapiens GN=GJA9 PE=2 SV=2 - [CXA9_HUMAN]
Q6PEY0	Gap junction beta-7 protein OS=Homo sapiens GN=GJB7 PE=2 SV=1 - [CXB7_HUMAN]
Q86XJ1	GAS2-like protein 3 OS=Homo sapiens GN=GAS2L3 PE=1 SV=1 - [GA2L3_HUMAN]
P32239	Gastrin/cholecystokinin type B receptor OS=Homo sapiens GN=CCKBR PE=1 SV=1 - [GASR_HUMAN]
P0CG01	Gastrokine-3 OS=Homo sapiens GN=GKN3P PE=3 SV=1 - [GKN3_HUMAN]

P57678	Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=2 - [GEMI4_HUMAN]
Q12789	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 - [TF3C1_HUMAN]
P78347	General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 - [GTF2I_HUMAN]
O60763	General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2 - [USO1_HUMAN]
Q14687	Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3 - [GSE1_HUMAN]
O60318	Germinal-center associated nuclear protein OS=Homo sapiens GN=MCM3AP PE=1 SV=2 - [GANP_HUMAN]
Q3V6T2	Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2 - [GRDN_HUMAN]
P07093	Glia-derived nexin OS=Homo sapiens GN=SERPINE2 PE=1 SV=1 - [GDN_HUMAN]
Q6ZMI3	Gliomedin OS=Homo sapiens GN=GLDN PE=2 SV=1 - [GLDN_HUMAN]
O95838	Glucagon-like peptide 2 receptor OS=Homo sapiens GN=GLP2R PE=2 SV=1 - [GLP2R_HUMAN]
P04150	Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=1 SV=1 - [GCR_HUMAN]
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]
Q4G148	Glucoside xylosyltransferase 1 OS=Homo sapiens GN=GXYLT1 PE=1 SV=2 - [GXLT1_HUMAN]
A0PJZ3	Glucoside xylosyltransferase 2 OS=Homo sapiens GN=GXYLT2 PE=2 SV=2 - [GXLT2_HUMAN]
Q13002	Glutamate receptor ionotropic, kainate 2 OS=Homo sapiens GN=GRIK2 PE=1 SV=1 - [GRIK2_HUMAN]
O15399	Glutamate receptor ionotropic, NMDA 2D OS=Homo sapiens GN=GRIN2D PE=1 SV=2 - [NMDE4_HUMAN]
Q86X53	Glutamate-rich protein 1 OS=Homo sapiens GN=ERICH1 PE=1 SV=1 - [ERIC1_HUMAN]
Q2KHR3	Glutamine and serine-rich protein 1 OS=Homo sapiens GN=QSER1 PE=1 SV=3 - [QSER1_HUMAN]
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]
Q9H0J4	Glutamine-rich protein 2 OS=Homo sapiens GN=QRICH2 PE=1 SV=1 - [QRIC2_HUMAN]
P47897	Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1 - [SYQ_HUMAN]
Q07075	Glutamyl aminopeptidase OS=Homo sapiens GN=ENPEP PE=1 SV=3 - [AMPE_HUMAN]
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]
Q8NEC7	Glutathione S-transferase C-terminal domain-containing protein OS=Homo sapiens GN=GSTCD PE=1 SV=2 - [GSTCD_HUMAN]
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1 - [GPD1L_HUMAN]
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]
P13807	Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2 - [GYS1_HUMAN]
P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]
P11217	Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 - [PYGM_HUMAN]
Q9NU53	Glycoprotein integral membrane protein 1 OS=Homo sapiens GN=GINM1 PE=2 SV=1 - [GINM1_HUMAN]
Q9H1C3	Glycosyltransferase 8 domain-containing protein 2 OS=Homo sapiens GN=GLT8D2 PE=2 SV=1 - [GL8D2_HUMAN]
Q13439	Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4 PE=1 SV=1 - [GOGA4_HUMAN]
Q14789	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2 - [GOGB1_HUMAN]
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN]
Q75T13	GPI inositol-deacylase OS=Homo sapiens GN=PGAP1 PE=1 SV=1 - [PGAP1_HUMAN]
Q9NUD9	GPI mannosyltransferase 2 OS=Homo sapiens GN=PIGV PE=1 SV=1 - [PIGV_HUMAN]
Q969N2	GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=1 SV=1 - [PIGT_HUMAN]
Q96PE1	G-protein coupled receptor 124 OS=Homo sapiens GN=GPR124 PE=1 SV=2 - [GP124_HUMAN]
P51810	G-protein coupled receptor 143 OS=Homo sapiens GN=GPR143 PE=1 SV=2 - [GP143_HUMAN]
P32249	G-protein coupled receptor 183 OS=Homo sapiens GN=GPR183 PE=1 SV=3 - [GP183_HUMAN]
Q8WXG9	G-protein coupled receptor 98 OS=Homo sapiens GN=GPR98 PE=1 SV=2 - [GPR98_HUMAN]
Q96D09	G-protein coupled receptor-associated sorting protein 2 OS=Homo sapiens GN=GPRASP2 PE=1 SV=1 - [GASP2_HUMAN]
Q96CP6	GRAM domain-containing protein 1A OS=Homo sapiens GN=GRAMD1A PE=1 SV=2 - [GRM1A_HUMAN]
Q96HH9	GRAM domain-containing protein 3 OS=Homo sapiens GN=GRAMD3 PE=1 SV=1 - [GRAM3_HUMAN]
Q8IWJ2	GRIP and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=GCC2 PE=1 SV=4 - [GCC2_HUMAN]
Q92847	Growth hormone secretagogue receptor type 1 OS=Homo sapiens GN=GHSR PE=1 SV=1 - [GHSR_HUMAN]
P43026	Growth/differentiation factor 5 OS=Homo sapiens GN=GDF5 PE=1 SV=3 - [GDF5_HUMAN]

Q7Z4P5	Growth/differentiation factor 7 OS=Homo sapiens GN=GDF7 PE=2 SV=2 - [GDF7_HUMAN]
O14793	Growth/differentiation factor 8 OS=Homo sapiens GN=MSTN PE=1 SV=1 - [GDF8_HUMAN]
Q9HAV7	GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2 - [GRPE1_HUMAN]
Q6P9H5	GTPase IMAP family member 6 OS=Homo sapiens GN=GIMAP6 PE=2 SV=1 - [GIMA6_HUMAN]
Q8NHV1	GTPase IMAP family member 7 OS=Homo sapiens GN=GIMAP7 PE=1 SV=1 - [GIMA7_HUMAN]
Q8ND71	GTPase IMAP family member 8 OS=Homo sapiens GN=GIMAP8 PE=2 SV=2 - [GIMA8_HUMAN]
Q8IYK8	GTP-binding protein REM 2 OS=Homo sapiens GN=REM2 PE=1 SV=2 - [REM2_HUMAN]
Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2 - [GNAS1_HUMAN]
P11488	Guanine nucleotide-binding protein G(t) subunit alpha-1 OS=Homo sapiens GN=GNAT1 PE=1 SV=5 - [GNAT1_HUMAN]
P30679	Guanine nucleotide-binding protein subunit alpha-15 OS=Homo sapiens GN=GNA15 PE=1 SV=2 - [GNA15_HUMAN]
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3 - [GBB4_HUMAN]
P36915	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2 - [GNL1_HUMAN]
P33402	Guanylate cyclase soluble subunit alpha-2 OS=Homo sapiens GN=GUCY1A2 PE=2 SV=1 - [GCYA2_HUMAN]
Q16774	Guanylate kinase OS=Homo sapiens GN=GUK1 PE=1 SV=2 - [KGUA_HUMAN]
P51795	H(+)/Cl(-) exchange transporter 5 OS=Homo sapiens GN=CLCN5 PE=1 SV=1 - [CLCN5_HUMAN]
P00738	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1 - [HPT_HUMAN]
Q9H6D7	HAUS augmin-like complex subunit 4 OS=Homo sapiens GN=HAUS4 PE=1 SV=1 - [HAUS4_HUMAN]
Q99871	HAUS augmin-like complex subunit 7 OS=Homo sapiens GN=HAUS7 PE=1 SV=3 - [HAUS7_HUMAN]
Q9Y450	HBS1-like protein OS=Homo sapiens GN=HBS1L PE=1 SV=1 - [HBS1L_HUMAN]
Q9UBI9	Headcase protein homolog OS=Homo sapiens GN=HECA PE=1 SV=1 - [HDC_HUMAN]
O43301	Heat shock 70 kDa protein 12A OS=Homo sapiens GN=HSPA12A PE=1 SV=2 - [HS12A_HUMAN]
O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]
O75031	Heat shock factor 2-binding protein OS=Homo sapiens GN=HSF2BP PE=1 SV=1 - [HSF2B_HUMAN]
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]
Q9Y4B4	Helicase ARIP4 OS=Homo sapiens GN=RAD54L2 PE=1 SV=4 - [ARIP4_HUMAN]
Q15477	Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=1 SV=3 - [SKIV2_HUMAN]
Q6ZRS2	Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3 - [SRCAP_HUMAN]
P14317	Hematopoietic lineage cell-specific protein OS=Homo sapiens GN=HCLS1 PE=1 SV=3 - [HCLS1_HUMAN]
P09601	Heme oxygenase 1 OS=Homo sapiens GN=HMOX1 PE=1 SV=1 - [HMOX1_HUMAN]
Q96RW7	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2 - [HMCN1_HUMAN]
Q8NDA2	Hemicentin-2 OS=Homo sapiens GN=HMCN2 PE=2 SV=2 - [HMCN2_HUMAN]
Q9Y5R4	HemK methyltransferase family member 1 OS=Homo sapiens GN=HEMK1 PE=1 SV=1 - [HEMK1_HUMAN]
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 - [HBA_HUMAN]
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 - [HBB_HUMAN]
Q96MM7	Heparan-sulfate 6-O-sulfotransferase 2 OS=Homo sapiens GN=HS6ST2 PE=2 SV=2 - [H6ST2_HUMAN]
Q14541	Hepatocyte nuclear factor 4-gamma OS=Homo sapiens GN=HNF4G PE=1 SV=3 - [HNF4G_HUMAN]
Q5TGJ6	Hepatoma-derived growth factor-like protein 1 OS=Homo sapiens GN=HDGFL1 PE=2 SV=1 - [HDGL1_HUMAN]
Q9UPZ3	Hermansky-Pudlak syndrome 5 protein OS=Homo sapiens GN=HPS5 PE=1 SV=2 - [HPS5_HUMAN]
Q86YV9	Hermansky-Pudlak syndrome 6 protein OS=Homo sapiens GN=HPS6 PE=1 SV=1 - [HPS6_HUMAN]
Q9N2J8	HERV-H_2q24.1 provirus ancestral Env polyprotein OS=Homo sapiens PE=2 SV=1 - [ENH3_HUMAN]
Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 - [HNRPD_HUMAN]
O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 - [HNRDL_HUMAN]
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HUMAN]
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_HUMAN]
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 -

	[HNRPC_HUMAN]
Q6UWX4	HHIP-like protein 2 OS=Homo sapiens GN=HHIPL2 PE=1 SV=1 - [HIPL2_HUMAN]
Q01362	High affinity immunoglobulin epsilon receptor subunit beta OS=Homo sapiens GN=MS4A2 PE=2 SV=1 - [FCERB_HUMAN]
P82970	High mobility group nucleosome-binding domain-containing protein 5 OS=Homo sapiens GN=HMGN5 PE=1 SV=1 - [HMGN5_HUMAN]
P17096	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3 - [HMGA1_HUMAN]
Q9BW71	HIRA-interacting protein 3 OS=Homo sapiens GN=HIRIP3 PE=1 SV=3 - [HIRP3_HUMAN]
Q9Y5N1	Histamine H3 receptor OS=Homo sapiens GN=HRH3 PE=1 SV=2 - [HRH3_HUMAN]
P19113	Histidine decarboxylase OS=Homo sapiens GN=HDC PE=1 SV=2 - [DCHS_HUMAN]
Q92830	Histone acetyltransferase KAT2A OS=Homo sapiens GN=KAT2A PE=1 SV=3 - [KAT2A_HUMAN]
Q92831	Histone acetyltransferase KAT2B OS=Homo sapiens GN=KAT2B PE=1 SV=3 - [KAT2B_HUMAN]
Q92993	Histone acetyltransferase KAT5 OS=Homo sapiens GN=KAT5 PE=1 SV=2 - [KAT5_HUMAN]
Q8WYB5	Histone acetyltransferase KAT6B OS=Homo sapiens GN=KAT6B PE=1 SV=3 - [KAT6B_HUMAN]
O95251	Histone acetyltransferase KAT7 OS=Homo sapiens GN=KAT7 PE=1 SV=1 - [KAT7_HUMAN]
Q09472	Histone acetyltransferase p300 OS=Homo sapiens GN=EP300 PE=1 SV=2 - [EP300_HUMAN]
Q92769	Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2 - [HDAC2_HUMAN]
Q9UQL6	Histone deacetylase 5 OS=Homo sapiens GN=HDAC5 PE=1 SV=2 - [HDAC5_HUMAN]
Q9UKV0	Histone deacetylase 9 OS=Homo sapiens GN=HDAC9 PE=1 SV=2 - [HDAC9_HUMAN]
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]
Q5VVJ2	Histone H2A deubiquitinase MYSM1 OS=Homo sapiens GN=MYSM1 PE=1 SV=1 - [MYSM1_HUMAN]
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]
Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4 - [H2A2C_HUMAN]
P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3 - [H2B1O_HUMAN]
Q6NXT2	Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3 - [H3C_HUMAN]
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]
Q9UMN6	Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1 - [KMT2B_HUMAN]
Q8NEZ4	Histone-lysine N-methyltransferase 2C OS=Homo sapiens GN=KMT2C PE=1 SV=3 - [KMT2C_HUMAN]
O14686	Histone-lysine N-methyltransferase 2D OS=Homo sapiens GN=KMT2D PE=1 SV=2 - [KMT2D_HUMAN]
Q8IZD2	Histone-lysine N-methyltransferase 2E OS=Homo sapiens GN=KMT2E PE=1 SV=1 - [KMT2E_HUMAN]
Q92800	Histone-lysine N-methyltransferase EZH1 OS=Homo sapiens GN=EZH1 PE=1 SV=2 - [EZH1_HUMAN]
O15047	Histone-lysine N-methyltransferase SETD1A OS=Homo sapiens GN=SETD1A PE=1 SV=3 - [SET1A_HUMAN]
Q9BYW2	Histone-lysine N-methyltransferase SETD2 OS=Homo sapiens GN=SETD2 PE=1 SV=3 - [SETD2_HUMAN]
Q15047	Histone-lysine N-methyltransferase SETDB1 OS=Homo sapiens GN=SETDB1 PE=1 SV=1 - [SETB1_HUMAN]
Q96T68	Histone-lysine N-methyltransferase SETDB2 OS=Homo sapiens GN=SETDB2 PE=1 SV=2 - [SETB2_HUMAN]
O43463	Histone-lysine N-methyltransferase SUV39H1 OS=Homo sapiens GN=SUV39H1 PE=1 SV=1 - [SUV91_HUMAN]
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOT1L PE=1 SV=2 - [DOT1L_HUMAN]
P30511	HLA class I histocompatibility antigen, alpha chain F OS=Homo sapiens GN=HLA-F PE=2 SV=3 - [HLAF_HUMAN]
P01909	HLA class II histocompatibility antigen, DQ alpha 1 chain OS=Homo sapiens GN=HLA-DQA1 PE=1 SV=1 - [DQA1_HUMAN]
P05538	HLA class II histocompatibility antigen, DQ beta 2 chain OS=Homo sapiens GN=HLA-DQB2 PE=1 SV=2 - [DQB2_HUMAN]
Q12766	HMG domain-containing protein 3 OS=Homo sapiens GN=HMGXB3 PE=2 SV=2 - [HMGX3_HUMAN]
P47902	Homeobox protein CDX-1 OS=Homo sapiens GN=CDX1 PE=1 SV=2 - [CDX1_HUMAN]
P39880	Homeobox protein cut-like 1 OS=Homo sapiens GN=CUX1 PE=1 SV=3 - [CUX1_HUMAN]
Q9NYD6	Homeobox protein Hox-C10 OS=Homo sapiens GN=HOXC10 PE=1 SV=2 - [HXC10_HUMAN]
P52952	Homeobox protein Nkx-2.5 OS=Homo sapiens GN=NKX2-5 PE=1 SV=1 - [NKX25_HUMAN]
Q99801	Homeobox protein Nkx-3.1 OS=Homo sapiens GN=NKX3-1 PE=1 SV=2 - [NKX31_HUMAN]
Q8IUE1	Homeobox protein TGIF2LX OS=Homo sapiens GN=TGIF2LX PE=1 SV=1 - [TF2LX_HUMAN]
Q05469	Hormone-sensitive lipase OS=Homo sapiens GN=LIPE PE=1 SV=4 - [LIPS_HUMAN]
P51610	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]

P53816	HRAS-like suppressor 3 OS=Homo sapiens GN=PLA2G16 PE=1 SV=2 - [HRSL3_HUMAN]
P0CJ69	Humanin-like 2 OS=Homo sapiens GN=MTRNR2L2 PE=2 SV=1 - [HMN2_HUMAN]
P42858	Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2 - [HD_HUMAN]
O00219	Hyaluronan synthase 3 OS=Homo sapiens GN=HAS3 PE=2 SV=3 - [HYAS3_HUMAN]
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]
P01857	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 - [IGHG1_HUMAN]
P01814	Ig heavy chain V-II region OU OS=Homo sapiens PE=1 SV=1 - [HV201_HUMAN]
P01834	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 - [IGKC_HUMAN]
P01620	Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1 - [KV302_HUMAN]
P01706	Ig lambda chain V-II region BOH OS=Homo sapiens PE=1 SV=1 - [LV203_HUMAN]
P01708	Ig lambda chain V-II region BUR OS=Homo sapiens PE=1 SV=1 - [LV205_HUMAN]
Q8WZA9	Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1 - [IRGQ_HUMAN]
P01591	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4 - [IGJ_HUMAN]
Q6WRI0	Immunoglobulin superfamily member 10 OS=Homo sapiens GN=IGSF10 PE=2 SV=1 - [IGS10_HUMAN]
Q93033	Immunoglobulin superfamily member 2 OS=Homo sapiens GN=CD101 PE=1 SV=2 - [IGSF2_HUMAN]
O75054	Immunoglobulin superfamily member 3 OS=Homo sapiens GN=IGSF3 PE=2 SV=3 - [IGSF3_HUMAN]
Q969P0	Immunoglobulin superfamily member 8 OS=Homo sapiens GN=IGSF8 PE=1 SV=1 - [IGSF8_HUMAN]
Q86VF2	Immunoglobulin-like and fibronectin type III domain-containing protein 1 OS=Homo sapiens GN=IGFN1 PE=1 SV=2 - [IGFN1_HUMAN]
Q8TEX9	Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2 - [IPO4_HUMAN]
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]
Q8N608	Inactive dipeptidyl peptidase 10 OS=Homo sapiens GN=DPP10 PE=1 SV=2 - [DPP10_HUMAN]
Q7Z4T8	Inactive polypeptide N-acetylgalactosaminyltransferase-like protein 5 OS=Homo sapiens GN=GALNTL5 PE=2 SV=3 - [GLTL5_HUMAN]
Q8NI35	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3 - [INADL_HUMAN]
P20839	Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=1 SV=2 - [IMDH1_HUMAN]
Q6GPH6	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 1 OS=Homo sapiens GN=ITPRIPL1 PE=1 SV=1 - [IPIL1_HUMAN]
P23677	Inositol-trisphosphate 3-kinase A OS=Homo sapiens GN=ITPKA PE=1 SV=1 - [IP3KA_HUMAN]
Q96DU7	Inositol-trisphosphate 3-kinase C OS=Homo sapiens GN=ITPKC PE=1 SV=1 - [IP3KC_HUMAN]
Q9Y4H2	Insulin receptor substrate 2 OS=Homo sapiens GN=IRS2 PE=1 SV=2 - [IRS2_HUMAN]
O14654	Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1 - [IRS4_HUMAN]
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2 - [IF2B1_HUMAN]
P08833	Insulin-like growth factor-binding protein 1 OS=Homo sapiens GN=IGFBP1 PE=1 SV=1 - [IBP1_HUMAN]
Q86V85	Integral membrane protein GPR180 OS=Homo sapiens GN=GPR180 PE=2 SV=1 - [GP180_HUMAN]
Q8N201	Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2 - [INT1_HUMAN]
Q9NVH2	Integrator complex subunit 7 OS=Homo sapiens GN=INTS7 PE=1 SV=1 - [INT7_HUMAN]
O75578	Integrin alpha-10 OS=Homo sapiens GN=ITGA10 PE=2 SV=2 - [ITA10_HUMAN]
P38570	Integrin alpha-E OS=Homo sapiens GN=ITGAE PE=1 SV=3 - [ITAE_HUMAN]
P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]
P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2 - [ITIH2_HUMAN]
Q9UMF0	Intercellular adhesion molecule 5 OS=Homo sapiens GN=ICAM5 PE=1 SV=3 - [ICAM5_HUMAN]
P17181	Interferon alpha/beta receptor 1 OS=Homo sapiens GN=IFNAR1 PE=1 SV=3 - [INAR1_HUMAN]
P01562	Interferon alpha-1/13 OS=Homo sapiens GN=IFNA1 PE=1 SV=1 - [IFNA1_HUMAN]
Q8IU57	Interferon lambda receptor 1 OS=Homo sapiens GN=IFNLR1 PE=1 SV=1 - [INLR1_HUMAN]
Q8IU81	Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens GN=IRF2BP1 PE=1 SV=1 - [I2BP1_HUMAN]
P20591	Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4 - [MX1_HUMAN]
Q9BYX4	Interferon-induced helicase C domain-containing protein 1 OS=Homo sapiens GN=IFIH1 PE=1 SV=3 - [IFIH1_HUMAN]
Q5T764	Interferon-induced protein with tetratricopeptide repeats 1B OS=Homo sapiens GN=IFIT1B PE=2 SV=1 - [IFT1B_HUMAN]
Q7Z2Y8	Interferon-induced very large GTPase 1 OS=Homo sapiens GN=GVINP1 PE=2 SV=2 - [GVIN1_HUMAN]
O00458	Interferon-related developmental regulator 1 OS=Homo sapiens GN=IFRD1 PE=1 SV=4 - [IFRD1_HUMAN]
Q9NPH3	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 - [IL1AP_HUMAN]

Q9Y616	Interleukin-1 receptor-associated kinase 3 OS=Homo sapiens GN=IRAK3 PE=1 SV=2 - [IRAK3_HUMAN]
Q16552	Interleukin-17A OS=Homo sapiens GN=IL17A PE=1 SV=1 - [IL17_HUMAN]
P14784	Interleukin-2 receptor subunit beta OS=Homo sapiens GN=IL2RB PE=1 SV=1 - [IL2RB_HUMAN]
Q5VWK5	Interleukin-23 receptor OS=Homo sapiens GN=IL23R PE=1 SV=3 - [IL23R_HUMAN]
Q6UWB1	Interleukin-27 receptor subunit alpha OS=Homo sapiens GN=IL27RA PE=2 SV=2 - [I27RA_HUMAN]
P05112	Interleukin-4 OS=Homo sapiens GN=IL4 PE=1 SV=1 - [IL4_HUMAN]
P16871	Interleukin-7 receptor subunit alpha OS=Homo sapiens GN=IL7R PE=1 SV=2 - [IL7RA_HUMAN]
Q9P2H3	Intraflagellar transport protein 80 homolog OS=Homo sapiens GN=IFT80 PE=1 SV=3 - [IFT80_HUMAN]
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 - [INF2_HUMAN]
Q8N2Y8	Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=3 - [RUSC2_HUMAN]
Q6IPM2	IQ domain-containing protein E OS=Homo sapiens GN=IQCE PE=1 SV=2 - [IQCE_HUMAN]
P0C7M6	IQ domain-containing protein F3 OS=Homo sapiens GN=IQCF3 PE=2 SV=1 - [IQCF3_HUMAN]
Q5JU85	IQ motif and SEC7 domain-containing protein 2 OS=Homo sapiens GN=IQSEC2 PE=1 SV=1 - [IQEC2_HUMAN]
P78414	Iroquois-class homeodomain protein IRX-1 OS=Homo sapiens GN=IRX1 PE=2 SV=3 - [IRX1_HUMAN]
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 - [IDH3A_HUMAN]
Q8N9B5	Junction-mediating and -regulatory protein OS=Homo sapiens GN=JMY PE=1 SV=2 - [JMY_HUMAN]
Q9HDC5	Junctophilin-1 OS=Homo sapiens GN=JPH1 PE=1 SV=2 - [JPH1_HUMAN]
O60229	Kalirin OS=Homo sapiens GN=KALRN PE=1 SV=2 - [KALRN_HUMAN]
O75449	Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens GN=KATNA1 PE=1 SV=1 - [KTNA1_HUMAN]
Q6PID8	Kelch domain-containing protein 10 OS=Homo sapiens GN=KLHDC10 PE=1 SV=1 - [KLD10_HUMAN]
Q9BQ90	Kelch domain-containing protein 3 OS=Homo sapiens GN=KLHDC3 PE=2 SV=1 - [KLDC3_HUMAN]
Q5VTJ3	Kelch domain-containing protein 7A OS=Homo sapiens GN=KLHDC7A PE=1 SV=5 - [KLD7A_HUMAN]
Q3ZCT8	Kelch repeat and BTB domain-containing protein 12 OS=Homo sapiens GN=KBTBD12 PE=2 SV=2 - [KBTBC_HUMAN]
Q8IY47	Kelch repeat and BTB domain-containing protein 2 OS=Homo sapiens GN=KBTBD2 PE=1 SV=2 - [KBTB2_HUMAN]
Q96M94	Kelch-like protein 15 OS=Homo sapiens GN=KLHL15 PE=1 SV=2 - [KLH15_HUMAN]
Q9UJP4	Kelch-like protein 21 OS=Homo sapiens GN=KLHL21 PE=1 SV=4 - [KLH21_HUMAN]
Q9H0H3	Kelch-like protein 25 OS=Homo sapiens GN=KLHL25 PE=1 SV=1 - [KLH25_HUMAN]
Q96CT2	Kelch-like protein 29 OS=Homo sapiens GN=KLHL29 PE=2 SV=3 - [KLH29_HUMAN]
Q8N4N3	Kelch-like protein 36 OS=Homo sapiens GN=KLHL36 PE=1 SV=1 - [KLH36_HUMAN]
Q2WGJ6	Kelch-like protein 38 OS=Homo sapiens GN=KLHL38 PE=1 SV=3 - [KLH38_HUMAN]
Q92764	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=5 - [KRT35_HUMAN]
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN]
P35900	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1 - [K1C20_HUMAN]
Q9C075	Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2 - [K1C23_HUMAN]
Q7Z3Z0	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN]
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]
P43628	Killer cell immunoglobulin-like receptor 2DL3 OS=Homo sapiens GN=KIR2DL3 PE=1 SV=1 - [KI2L3_HUMAN]
Q14943	Killer cell immunoglobulin-like receptor 3DS1 OS=Homo sapiens GN=KIR3DS1 PE=2 SV=1 - [KI3S1_HUMAN]
Q9ULH0	Kinase D-interacting substrate of 220 kDa OS=Homo sapiens GN=KIDINS220 PE=1 SV=3 - [KDIS_HUMAN]
Q8IVT5	Kinase suppressor of Ras 1 OS=Homo sapiens GN=KSR1 PE=1 SV=3 - [KSR1_HUMAN]
Q6VAB6	Kinase suppressor of Ras 2 OS=Homo sapiens GN=KSR2 PE=1 SV=2 - [KSR2_HUMAN]
Q12840	Kinesin heavy chain isoform 5A OS=Homo sapiens GN=KIF5A PE=1 SV=2 - [KIF5A_HUMAN]
O60282	Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1 - [KIF5C_HUMAN]
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]
P52732	Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2 - [KIF11_HUMAN]
Q96FN5	Kinesin-like protein KIF12 OS=Homo sapiens GN=KIF12 PE=1 SV=3 - [KIF12_HUMAN]

Q9NQT8	Kinesin-like protein KIF13B OS=Homo sapiens GN=KIF13B PE=1 SV=2 - [KI13B_HUMAN]
Q15058	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1 - [KIF14_HUMAN]
Q9NS87	Kinesin-like protein KIF15 OS=Homo sapiens GN=KIF15 PE=1 SV=1 - [KIF15_HUMAN]
Q8NI77	Kinesin-like protein KIF18A OS=Homo sapiens GN=KIF18A PE=1 SV=2 - [KI18A_HUMAN]
Q86Y91	Kinesin-like protein KIF18B OS=Homo sapiens GN=KIF18B PE=1 SV=3 - [KI18B_HUMAN]
Q12756	Kinesin-like protein KIF1A OS=Homo sapiens GN=KIF1A PE=1 SV=2 - [KIF1A_HUMAN]
O60333	Kinesin-like protein KIF1B OS=Homo sapiens GN=KIF1B PE=1 SV=5 - [KIF1B_HUMAN]
O43896	Kinesin-like protein KIF1C OS=Homo sapiens GN=KIF1C PE=1 SV=3 - [KIF1C_HUMAN]
Q96Q89	Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3 - [KI20B_HUMAN]
Q7Z4S6	Kinesin-like protein KIF21A OS=Homo sapiens GN=KIF21A PE=1 SV=2 - [KI21A_HUMAN]
Q5T7B8	Kinesin-like protein KIF24 OS=Homo sapiens GN=KIF24 PE=1 SV=2 - [KIF24_HUMAN]
Q9ULI4	Kinesin-like protein KIF26A OS=Homo sapiens GN=KIF26A PE=2 SV=3 - [KI26A_HUMAN]
Q2KJY2	Kinesin-like protein KIF26B OS=Homo sapiens GN=KIF26B PE=2 SV=1 - [KI26B_HUMAN]
Q86VH2	Kinesin-like protein KIF27 OS=Homo sapiens GN=KIF27 PE=2 SV=1 - [KIF27_HUMAN]
Q6ZMV9	Kinesin-like protein KIF6 OS=Homo sapiens GN=KIF6 PE=1 SV=3 - [KIF6_HUMAN]
Q9H410	Kinetochore-associated protein DSN1 homolog OS=Homo sapiens GN=DSN1 PE=1 SV=2 - [DSN1_HUMAN]
P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 - [KNG1_HUMAN]
Q14678	KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 PE=1 SV=3 - [KANK1_HUMAN]
Q63ZY3	KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1 - [KANK2_HUMAN]
Q8NCW0	Kremen protein 2 OS=Homo sapiens GN=KREMEN2 PE=2 SV=1 - [KREM2_HUMAN]
Q13601	KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1 PE=1 SV=4 - [KRR1_HUMAN]
Q9Y4X4	Krueppel-like factor 12 OS=Homo sapiens GN=KLF12 PE=1 SV=2 - [KLF12_HUMAN]
Q6PIL6	Kv channel-interacting protein 4 OS=Homo sapiens GN=KCNIP4 PE=1 SV=1 - [KCIP4_HUMAN]
Q9BYG0	Lactosylceramide 1,3-N-acetyl-beta-D-glucosaminyltransferase OS=Homo sapiens GN=B3GNT5 PE=1 SV=1 - [B3GN5_HUMAN]
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]
Q16363	Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=4 - [LAMA4_HUMAN]
O15230	Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8 - [LAMA5_HUMAN]
P55268	Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2 - [LAMB2_HUMAN]
A4D0S4	Laminin subunit beta-4 OS=Homo sapiens GN=LAMB4 PE=2 SV=1 - [LAMB4_HUMAN]
Q6PKG0	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 - [LARP1_HUMAN]
Q71RC2	La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3 - [LARP4_HUMAN]
Q9BRS8	La-related protein 6 OS=Homo sapiens GN=LARP6 PE=1 SV=1 - [LARP6_HUMAN]
Q14696	LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2 - [MESD_HUMAN]
O75610	Left-right determination factor 1 OS=Homo sapiens GN=LEFTY1 PE=2 SV=1 - [LFTY1_HUMAN]
Q68G75	LEM domain-containing protein 1 OS=Homo sapiens GN=LEMD1 PE=2 SV=2 - [LEMD1_HUMAN]
Q8NC56	LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1 - [LEMD2_HUMAN]
Q15334	Lethal(2) giant larvae protein homolog 1 OS=Homo sapiens GN=LLGL1 PE=1 SV=3 - [L2GL1_HUMAN]
Q2VYF4	LETM1 domain-containing protein LETM2, mitochondrial OS=Homo sapiens GN=LETM2 PE=2 SV=2 - [LETM2_HUMAN]
Q86V48	Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2 - [LUZP1_HUMAN]
Q9P127	Leucine zipper protein 4 OS=Homo sapiens GN=LUZP4 PE=1 SV=1 - [LUZP4_HUMAN]
Q9Y250	Leucine zipper putative tumor suppressor 1 OS=Homo sapiens GN=LZTS1 PE=1 SV=3 - [LZTS1_HUMAN]
Q6ZMV7	Leucine-, glutamate- and lysine-rich protein 1 OS=Homo sapiens GN=LEKR1 PE=2 SV=2 - [LEKR1_HUMAN]
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]
Q9C099	Leucine-rich repeat and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=LRRCC1 PE=1 SV=2 - [LRCC1_HUMAN]
Q9BTN0	Leucine-rich repeat and fibronectin type-III domain-containing protein 3 OS=Homo sapiens GN=LRFN3 PE=2 SV=1 - [LRFN3_HUMAN]
Q9Y608	Leucine-rich repeat flightless-interacting protein 2 OS=Homo sapiens GN=LRRFIP2 PE=1 SV=1 - [LRRF2_HUMAN]
O75325	Leucine-rich repeat neuronal protein 2 OS=Homo sapiens GN=LRRN2 PE=2 SV=2 - [LRRN2_HUMAN]
Q38SD2	Leucine-rich repeat serine/threonine-protein kinase 1 OS=Homo sapiens GN=LRRK1 PE=1 SV=3 - [LRRK1_HUMAN]

Q5S007	Leucine-rich repeat serine/threonine-protein kinase 2 OS=Homo sapiens GN=LRRK2 PE=1 SV=2 - [LRRK2_HUMAN]
O43300	Leucine-rich repeat transmembrane neuronal protein 2 OS=Homo sapiens GN=LRRTM2 PE=2 SV=3 - [LRRT2_HUMAN]
Q86VH4	Leucine-rich repeat transmembrane neuronal protein 4 OS=Homo sapiens GN=LRRTM4 PE=2 SV=2 - [LRRT4_HUMAN]
Q9P2V4	Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 1 OS=Homo sapiens GN=LRIT1 PE=2 SV=1 - [LRIT1_HUMAN]
A6NDA9	Leucine-rich repeat, immunoglobulin-like domain and transmembrane domain-containing protein 2 OS=Homo sapiens GN=LRIT2 PE=2 SV=1 - [LRIT2_HUMAN]
O75473	Leucine-rich repeat-containing G-protein coupled receptor 5 OS=Homo sapiens GN=LGR5 PE=1 SV=1 - [LGR5_HUMAN]
A6NIK2	Leucine-rich repeat-containing protein 10B OS=Homo sapiens GN=LRRC10B PE=4 SV=2 - [LR10B_HUMAN]
Q6F5E8	Leucine-rich repeat-containing protein 16C OS=Homo sapiens GN=RLTPR PE=1 SV=2 - [LR16C_HUMAN]
O60309	Leucine-rich repeat-containing protein 37A3 OS=Homo sapiens GN=LRRC37A3 PE=2 SV=2 - [L37A3_HUMAN]
Q9NT99	Leucine-rich repeat-containing protein 4B OS=Homo sapiens GN=LRRC4B PE=2 SV=3 - [LRC4B_HUMAN]
Q96CX6	Leucine-rich repeat-containing protein 58 OS=Homo sapiens GN=LRRC58 PE=1 SV=2 - [LRC58_HUMAN]
Q05C16	Leucine-rich repeat-containing protein 63 OS=Homo sapiens GN=LRRC63 PE=2 SV=2 - [LRC63_HUMAN]
Q5JTD7	Leucine-rich repeat-containing protein 73 OS=Homo sapiens GN=LRRC73 PE=2 SV=1 - [LRC73_HUMAN]
Q0VAA2	Leucine-rich repeat-containing protein 74A OS=Homo sapiens GN=LRRC74A PE=2 SV=2 - [LR74A_HUMAN]
Q96JA1	Leucine-rich repeats and immunoglobulin-like domains protein 1 OS=Homo sapiens GN=LRIG1 PE=1 SV=2 - [LRIG1_HUMAN]
O75023	Leukocyte immunoglobulin-like receptor subfamily B member 5 OS=Homo sapiens GN=LILRB5 PE=1 SV=1 - [LIRB5_HUMAN]
Q96BZ8	Leukocyte receptor cluster member 1 OS=Homo sapiens GN=LENG1 PE=1 SV=1 - [LENG1_HUMAN]
Q96PV6	Leukocyte receptor cluster member 8 OS=Homo sapiens GN=LENG8 PE=1 SV=2 - [LENG8_HUMAN]
Q08722	Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1 - [CD47_HUMAN]
P29376	Leukocyte tyrosine kinase receptor OS=Homo sapiens GN=LTK PE=1 SV=3 - [LTK_HUMAN]
Q8N3X6	Ligand-dependent nuclear receptor corepressor-like protein OS=Homo sapiens GN=LCORL PE=1 SV=4 - [LCORL_HUMAN]
Q9NZU5	LIM and cysteine-rich domains protein 1 OS=Homo sapiens GN=LMCD1 PE=1 SV=1 - [LMCD1_HUMAN]
Q8WWI1	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 - [LMO7_HUMAN]
Q8WVP7	Limb region 1 protein homolog OS=Homo sapiens GN=LMBR1 PE=1 SV=1 - [LMBR1_HUMAN]
O00370	LINE-1 retrotransposable element ORF2 protein OS=Homo sapiens PE=1 SV=1 - [LORF2_HUMAN]
Q96GM1	Lipid phosphate phosphatase-related protein type 2 OS=Homo sapiens GN=LPPR2 PE=2 SV=1 - [LPPR2_HUMAN]
Q7Z2D5	Lipid phosphate phosphatase-related protein type 4 OS=Homo sapiens GN=LPPR4 PE=1 SV=1 - [LPPR4_HUMAN]
O43688	Lipid phosphate phosphohydrolase 2 OS=Homo sapiens GN=PPAP2C PE=1 SV=1 - [LPP2_HUMAN]
Q86UP9	Lipoma HMGIC fusion partner-like 3 protein OS=Homo sapiens GN=LHFPL3 PE=2 SV=3 - [LHPL3_HUMAN]
P18428	Lipopolysaccharide-binding protein OS=Homo sapiens GN=LBP PE=1 SV=3 - [LBP_HUMAN]
O75334	Liprin-alpha-2 OS=Homo sapiens GN=PPFIA2 PE=1 SV=2 - [LIPA2_HUMAN]
O75145	Liprin-alpha-3 OS=Homo sapiens GN=PPFIA3 PE=1 SV=3 - [LIPA3_HUMAN]
Q9Y2F5	Little elongation complex subunit 1 OS=Homo sapiens GN=ICE1 PE=1 SV=5 - [ICE1_HUMAN]
Q8IVB5	LIX1-like protein OS=Homo sapiens GN=LIX1L PE=2 SV=1 - [LIX1L_HUMAN]
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]
Q1L5Z9	LON peptidase N-terminal domain and RING finger protein 2 OS=Homo sapiens GN=LONRF2 PE=2 SV=3 - [LONF2_HUMAN]
Q86WA8	Lon protease homolog 2, peroxisomal OS=Homo sapiens GN=LONP2 PE=1 SV=1 - [LONP2_HUMAN]
P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]
Q6PCB7	Long-chain fatty acid transport protein 1 OS=Homo sapiens GN=SLC27A1 PE=2 SV=1 - [S27A1_HUMAN]
Q9Y2P4	Long-chain fatty acid transport protein 6 OS=Homo sapiens GN=SLC27A6 PE=2 SV=1 - [S27A6_HUMAN]
Q96GR2	Long-chain-fatty-acid--CoA ligase ACSBG1 OS=Homo sapiens GN=ACSBG1 PE=2 SV=2 - [ACBG1_HUMAN]
P12318	Low affinity immunoglobulin gamma Fc region receptor II-a OS=Homo sapiens GN=FCGR2A PE=1 SV=4 - [FCG2A_HUMAN]
Q7Z4F1	Low-density lipoprotein receptor-related protein 10 OS=Homo sapiens GN=LRP10 PE=1 SV=2 - [LRP10_HUMAN]
Q9NZR2	Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2 - [LRP1B_HUMAN]
P98164	Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3 - [LRP2_HUMAN]

O95232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]
Q6UWN5	Ly6/PLAUR domain-containing protein 5 OS=Homo sapiens GN=LYPD5 PE=1 SV=2 - [LYPD5_HUMAN]
Q8NI32	Ly6/PLAUR domain-containing protein 6B OS=Homo sapiens GN=LYPD6B PE=2 SV=1 - [LPD6B_HUMAN]
O94772	Lymphocyte antigen 6H OS=Homo sapiens GN=LY6H PE=1 SV=1 - [LY6H_HUMAN]
O60449	Lymphocyte antigen 75 OS=Homo sapiens GN=LY75 PE=1 SV=3 - [LY75_HUMAN]
P47992	Lymphotactin OS=Homo sapiens GN=XCL1 PE=1 SV=1 - [XCL1_HUMAN]
P46736	Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2 - [BRCC3_HUMAN]
Q7LBC6	Lysine-specific demethylase 3B OS=Homo sapiens GN=KDM3B PE=1 SV=2 - [KDM3B_HUMAN]
O94953	Lysine-specific demethylase 4B OS=Homo sapiens GN=KDM4B PE=1 SV=4 - [KDM4B_HUMAN]
Q8N371	Lysine-specific demethylase 8 OS=Homo sapiens GN=KDM8 PE=1 SV=1 - [KDM8_HUMAN]
Q99677	Lysophosphatidic acid receptor 4 OS=Homo sapiens GN=LPAR4 PE=1 SV=1 - [LPAR4_HUMAN]
Q9H1C0	Lysophosphatidic acid receptor 5 OS=Homo sapiens GN=LPAR5 PE=2 SV=1 - [LPAR5_HUMAN]
Q6ZNC8	Lysophospholipid acyltransferase 1 OS=Homo sapiens GN=MBOAT1 PE=1 SV=1 - [MBOA1_HUMAN]
Q6ZP29	Lysosomal amino acid transporter 1 homolog OS=Homo sapiens GN=PQLC2 PE=1 SV=1 - [LAAT1_HUMAN]
P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]
Q15012	Lysosomal-associated transmembrane protein 4A OS=Homo sapiens GN=LAPTM4A PE=1 SV=1 - [LAP4A_HUMAN]
Q99698	Lysosomal-trafficking regulator OS=Homo sapiens GN=LYST PE=1 SV=3 - [LYST_HUMAN]
P39900	Macrophage metalloelastase OS=Homo sapiens GN=MMP12 PE=1 SV=1 - [MMP12_HUMAN]
Q9UEW3	Macrophage receptor MARCO OS=Homo sapiens GN=MARCO PE=1 SV=1 - [MARCO_HUMAN]
P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]
Q8NDA8	Maestro heat-like repeat-containing protein family member 1 OS=Homo sapiens GN=MROH1 PE=2 SV=3 - [MROH1_HUMAN]
Q7Z745	Maestro heat-like repeat-containing protein family member 2B OS=Homo sapiens GN=MROH2B PE=2 SV=3 - [MRO2B_HUMAN]
Q9HD23	Magnesium transporter MRS2 homolog, mitochondrial OS=Homo sapiens GN=MRS2 PE=1 SV=1 - [MRS2_HUMAN]
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]
Q68DK7	Male-specific lethal 1 homolog OS=Homo sapiens GN=MSL1 PE=1 SV=3 - [MSL1_HUMAN]
A6NHS7	MANSC domain-containing protein 4 OS=Homo sapiens GN=MANSC4 PE=3 SV=3 - [MANS4_HUMAN]
Q8WXG6	MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2 - [MADD_HUMAN]
P27448	MAP/microtubule affinity-regulating kinase 3 OS=Homo sapiens GN=MARK3 PE=1 SV=4 - [MARK3_HUMAN]
Q3KQU3	MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1 - [MA7D1_HUMAN]
Q8IWC1	MAP7 domain-containing protein 3 OS=Homo sapiens GN=MAP7D3 PE=1 SV=2 - [MA7D3_HUMAN]
Q96JK9	Mastermind-like protein 3 OS=Homo sapiens GN=MAML3 PE=1 SV=4 - [MAML3_HUMAN]
O15232	Matrilin-3 OS=Homo sapiens GN=MATN3 PE=1 SV=2 - [MATN3_HUMAN]
P51511	Matrix metalloproteinase-15 OS=Homo sapiens GN=MMP15 PE=1 SV=1 - [MMP15_HUMAN]
O75900	Matrix metalloproteinase-23 OS=Homo sapiens GN=MMP23A PE=1 SV=2 - [MMP23_HUMAN]
P14780	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 - [MMP9_HUMAN]
Q8IWI9	MAX gene-associated protein OS=Homo sapiens GN=MGA PE=1 SV=3 - [MGAP_HUMAN]
Q4G0Z9	MCM domain-containing protein 2 OS=Homo sapiens GN=MCMDC2 PE=1 SV=3 - [MCMD2_HUMAN]
Q5HYA8	Meckelin OS=Homo sapiens GN=TMEM67 PE=1 SV=2 - [MKS3_HUMAN]
Q15648	Mediator of RNA polymerase II transcription subunit 1 OS=Homo sapiens GN=MED1 PE=1 SV=4 - [MED1_HUMAN]
Q86YW9	Mediator of RNA polymerase II transcription subunit 12-like protein OS=Homo sapiens GN=MED12L PE=1 SV=2 - [MD12L_HUMAN]
O75448	Mediator of RNA polymerase II transcription subunit 24 OS=Homo sapiens GN=MED24 PE=1 SV=1 - [MED24_HUMAN]
P42679	Megakaryocyte-associated tyrosine-protein kinase OS=Homo sapiens GN=MATK PE=1 SV=1 - [MATK_HUMAN]
Q9Y4F3	Meiosis arrest female protein 1 OS=Homo sapiens GN=KIAA0430 PE=1 SV=6 - [MARF1_HUMAN]
A0A087WXM9	Meiosis-specific kinetochore protein OS=Homo sapiens GN=MEIKIN PE=2 SV=2 - [MEIKN_HUMAN]
Q5JRA6	Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1 - [MIA3_HUMAN]
Q9UNF1	Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2 - [MAGD2_HUMAN]
Q96QZ7	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1 OS=Homo sapiens GN=MAGI1 PE=1 SV=3 - [MAGI1_HUMAN]
Q86UL8	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 OS=Homo sapiens

	GN=MAGI2 PE=1 SV=3 - [MAGI2_HUMAN]
Q14703	Membrane-bound transcription factor site-1 protease OS=Homo sapiens GN=MBTPS1 PE=1 SV=1 - [MBTP1_HUMAN]
Q13421	Mesothelin OS=Homo sapiens GN=MSLN PE=1 SV=2 - [MSLN_HUMAN]
Q13255	Metabotropic glutamate receptor 1 OS=Homo sapiens GN=GRM1 PE=1 SV=3 - [GRM1_HUMAN]
Q14416	Metabotropic glutamate receptor 2 OS=Homo sapiens GN=GRM2 PE=1 SV=2 - [GRM2_HUMAN]
O15303	Metabotropic glutamate receptor 6 OS=Homo sapiens GN=GRM6 PE=1 SV=2 - [GRM6_HUMAN]
Q9UHE8	Metalloreductase STEAP1 OS=Homo sapiens GN=STEAP1 PE=2 SV=1 - [STEA1_HUMAN]
Q6ZN28	Metastasis-associated in colon cancer protein 1 OS=Homo sapiens GN=MACC1 PE=1 SV=2 - [MACC1_HUMAN]
O94776	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1 - [MTA2_HUMAN]
P53582	Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2 - [MAP11_HUMAN]
P50579	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 - [MAP2_HUMAN]
Q9UBK8	Methionine synthase reductase OS=Homo sapiens GN=MTRR PE=1 SV=3 - [MTRR_HUMAN]
Q8NHZ7	Methyl-CpG-binding domain protein 3-like 2 OS=Homo sapiens GN=MBD3L2 PE=2 SV=3 - [MB3L2_HUMAN]
Q6N021	Methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=3 - [TET2_HUMAN]
O43151	Methylcytosine dioxygenase TET3 OS=Homo sapiens GN=TET3 PE=1 SV=3 - [TET3_HUMAN]
Q13825	Methylglutaconyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=AUH PE=1 SV=1 - [AUHM_HUMAN]
Q8IVH4	Methylmalonic aciduria type A protein, mitochondrial OS=Homo sapiens GN=MMAA PE=1 SV=1 - [MMAA_HUMAN]
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 - [MEP50_HUMAN]
Q9NX63	MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1 - [MIC19_HUMAN]
Q8NEM0	Microcephalin OS=Homo sapiens GN=MCPH1 PE=1 SV=3 - [MCPH1_HUMAN]
Q96EZ8	Microspherule protein 1 OS=Homo sapiens GN=MCRS1 PE=1 SV=1 - [MCRS1_HUMAN]
Q9Y4B5	Microtubule cross-linking factor 1 OS=Homo sapiens GN=MTCL1 PE=1 SV=5 - [MTCL1_HUMAN]
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 - [MACF1_HUMAN]
Q9P2G4	Microtubule-associated protein 10 OS=Homo sapiens GN=MAP10 PE=1 SV=2 - [MAP10_HUMAN]
P78559	Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=6 - [MAP1A_HUMAN]
Q96JE9	Microtubule-associated protein 6 OS=Homo sapiens GN=MAP6 PE=1 SV=2 - [MAP6_HUMAN]
Q6P0Q8	Microtubule-associated serine/threonine-protein kinase 2 OS=Homo sapiens GN=MAST2 PE=1 SV=2 - [MAST2_HUMAN]
O60307	Microtubule-associated serine/threonine-protein kinase 3 OS=Homo sapiens GN=MAST3 PE=1 SV=2 - [MAST3_HUMAN]
Q9ULD2	Microtubule-associated tumor suppressor 1 OS=Homo sapiens GN=MTUS1 PE=1 SV=2 - [MTUS1_HUMAN]
Q6P0N0	Mis18-binding protein 1 OS=Homo sapiens GN=MIS18BP1 PE=1 SV=1 - [M18BP_HUMAN]
Q8TC71	Mitochondria-eating protein OS=Homo sapiens GN=SPATA18 PE=1 SV=1 - [MIEAP_HUMAN]
Q7Z434	Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 - [MAVS_HUMAN]
Q96C03	Mitochondrial dynamics protein MID49 OS=Homo sapiens GN=MIEF2 PE=1 SV=1 - [MID49_HUMAN]
Q9NQG6	Mitochondrial dynamics protein MID51 OS=Homo sapiens GN=MIEF1 PE=1 SV=1 - [MID51_HUMAN]
Q7L5Y1	Mitochondrial enolase superfamily member 1 OS=Homo sapiens GN=ENOSF1 PE=1 SV=1 - [ENOF1_HUMAN]
Q9UDX5	Mitochondrial fission process protein 1 OS=Homo sapiens GN=MTFP1 PE=1 SV=1 - [MTFP1_HUMAN]
Q6P444	Mitochondrial fission regulator 2 OS=Homo sapiens GN=MTFR2 PE=1 SV=2 - [MTFR2_HUMAN]
O14925	Mitochondrial import inner membrane translocase subunit Tim23 OS=Homo sapiens GN=TIMM23 PE=1 SV=1 - [TIM23_HUMAN]
Q9BT17	Mitochondrial ribosome-associated GTPase 1 OS=Homo sapiens GN=MTG1 PE=1 SV=2 - [MTG1_HUMAN]
O95140	Mitofusin-2 OS=Homo sapiens GN=MFN2 PE=1 SV=3 - [MFN2_HUMAN]
Q13233	Mitogen-activated protein kinase kinase kinase 1 OS=Homo sapiens GN=MAP3K1 PE=1 SV=4 - [M3K1_HUMAN]
Q02779	Mitogen-activated protein kinase kinase kinase 10 OS=Homo sapiens GN=MAP3K10 PE=1 SV=3 - [M3K10_HUMAN]
Q16584	Mitogen-activated protein kinase kinase kinase 11 OS=Homo sapiens GN=MAP3K11 PE=1 SV=1 - [M3K11_HUMAN]
Q99558	Mitogen-activated protein kinase kinase kinase 14 OS=Homo sapiens GN=MAP3K14 PE=1 SV=2 - [M3K14_HUMAN]
Q56UN5	Mitogen-activated protein kinase kinase kinase 19 OS=Homo sapiens GN=MAP3K19 PE=2 SV=1 - [M3K19_HUMAN]
Q99683	Mitogen-activated protein kinase kinase kinase 5 OS=Homo sapiens GN=MAP3K5 PE=1 SV=1 - [M3K5_HUMAN]

Q12851	Mitogen-activated protein kinase kinase kinase kinase 2 OS=Homo sapiens GN=MAP4K2 PE=1 SV=2 - [M4K2_HUMAN]
O95819	Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2 - [M4K4_HUMAN]
O60336	Mitogen-activated protein kinase-binding protein 1 OS=Homo sapiens GN=MAPKBP1 PE=1 SV=4 - [MABP1_HUMAN]
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Homo sapiens GN=BUB1B PE=1 SV=3 - [BUB1B_HUMAN]
Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens GN=MAD1L1 PE=1 SV=2 - [MD1L1_HUMAN]
Q96BY2	Modulator of apoptosis 1 OS=Homo sapiens GN=MOAP1 PE=1 SV=1 - [MOAP1_HUMAN]
O15374	Monocarboxylate transporter 5 OS=Homo sapiens GN=SLC16A4 PE=2 SV=1 - [MOT5_HUMAN]
Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1 - [C1TM_HUMAN]
Q15014	Mortality factor 4-like protein 2 OS=Homo sapiens GN=MORF4L2 PE=1 SV=1 - [MO4L2_HUMAN]
Q8NHP6	Motile sperm domain-containing protein 2 OS=Homo sapiens GN=MOSPD2 PE=1 SV=1 - [MSPD2_HUMAN]
Q99549	M-phase phosphoprotein 8 OS=Homo sapiens GN=MPHOSPH8 PE=1 SV=2 - [MPP8_HUMAN]
Q8WXI7	Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2 - [MUC16_HUMAN]
Q7Z5P9	Mucin-19 OS=Homo sapiens GN=MUC19 PE=1 SV=2 - [MUC19_HUMAN]
Q02817	Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2 - [MUC2_HUMAN]
Q9H195	Mucin-3B (Fragments) OS=Homo sapiens GN=MUC3B PE=2 SV=2 - [MUC3B_HUMAN]
P08183	Multidrug resistance protein 1 OS=Homo sapiens GN=ABCB1 PE=1 SV=3 - [MDR1_HUMAN]
P33527	Multidrug resistance-associated protein 1 OS=Homo sapiens GN=ABCC1 PE=1 SV=3 - [MRP1_HUMAN]
O95255	Multidrug resistance-associated protein 6 OS=Homo sapiens GN=ABCC6 PE=1 SV=2 - [MRP6_HUMAN]
Q6DN12	Multiple C2 and transmembrane domain-containing protein 2 OS=Homo sapiens GN=MCTP2 PE=1 SV=3 - [MCTP2_HUMAN]
Q96KG7	Multiple epidermal growth factor-like domains protein 10 OS=Homo sapiens GN=MEGF10 PE=1 SV=1 - [MEG10_HUMAN]
O75970	Multiple PDZ domain protein OS=Homo sapiens GN=MPDZ PE=1 SV=2 - [MPDZ_HUMAN]
P20309	Muscarinic acetylcholine receptor M3 OS=Homo sapiens GN=CHRM3 PE=1 SV=1 - [ACM3_HUMAN]
Q9NUK0	Muscleblind-like protein 3 OS=Homo sapiens GN=MBNL3 PE=1 SV=2 - [MBNL3_HUMAN]
O15457	MutS protein homolog 4 OS=Homo sapiens GN=MSH4 PE=1 SV=2 - [MSH4_HUMAN]
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]
P10244	Myb-related protein B OS=Homo sapiens GN=MYBL2 PE=1 SV=1 - [MYBB_HUMAN]
O00499	Myc box-dependent-interacting protein 1 OS=Homo sapiens GN=BIN1 PE=1 SV=1 - [BIN1_HUMAN]
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1 - [ABHDA_HUMAN]
Q9Y2G1	Myelin regulatory factor OS=Homo sapiens GN=MYRF PE=1 SV=3 - [MRF_HUMAN]
Q96LU7	Myelin regulatory factor-like protein OS=Homo sapiens GN=MYRFL PE=2 SV=2 - [MRFL_HUMAN]
Q9UL68	Myelin transcription factor 1-like protein OS=Homo sapiens GN=MYT1L PE=2 SV=3 - [MYT1L_HUMAN]
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]
Q8IZQ8	Myocardin OS=Homo sapiens GN=MYOCD PE=1 SV=1 - [MYCD_HUMAN]
Q5VU43	Myomegalin OS=Homo sapiens GN=PDE4DIP PE=1 SV=1 - [MYOME_HUMAN]
Q15746	Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4 - [MYLK_HUMAN]
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]
Q6WCQ1	Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP PE=1 SV=3 - [MPRIP_HUMAN]
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]
Q9Y2K3	Myosin-15 OS=Homo sapiens GN=MYH15 PE=1 SV=5 - [MYH15_HUMAN]
Q9Y623	Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2 - [MYH4_HUMAN]
A7E2Y1	Myosin-7B OS=Homo sapiens GN=MYH7B PE=1 SV=3 - [MYH7B_HUMAN]
P13535	Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3 - [MYH8_HUMAN]
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]
Q14896	Myosin-binding protein C, cardiac-type OS=Homo sapiens GN=MYBPC3 PE=1 SV=4 - [MYPC3_HUMAN]
Q00872	Myosin-binding protein C, slow-type OS=Homo sapiens GN=MYBPC1 PE=1 SV=2 - [MYPC1_HUMAN]
A2RUH7	Myosin-binding protein H-like OS=Homo sapiens GN=MYBPHL PE=1 SV=2 - [MBPHL_HUMAN]
Q8NEV4	Myosin-IIIa OS=Homo sapiens GN=MYO3A PE=2 SV=2 - [MYO3A_HUMAN]
Q9NXD2	Myotubularin-related protein 10 OS=Homo sapiens GN=MTMR10 PE=1 SV=3 - [MTMRA_HUMAN]
A4FU01	Myotubularin-related protein 11 OS=Homo sapiens GN=MTMR11 PE=2 SV=2 - [MTMRB_HUMAN]

Q9Y216	Myotubularin-related protein 7 OS=Homo sapiens GN=MTMR7 PE=1 SV=3 - [MTMR7_HUMAN]
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]
Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2 - [NHRF2_HUMAN]
Q76KP1	N-acetyl-beta-glucosaminyl-glycoprotein 4-beta-N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=B4GALNT4 PE=1 SV=1 - [B4GN4_HUMAN]
Q9UJ70	N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4 - [NAGK_HUMAN]
Q9ULI1	NACHT and WD repeat domain-containing protein 2 OS=Homo sapiens GN=NWD2 PE=2 SV=3 - [NWD2_HUMAN]
Q149M9	NACHT domain- and WD repeat-containing protein 1 OS=Homo sapiens GN=NWD1 PE=1 SV=3 - [NWD1_HUMAN]
Q9C000	NACHT, LRR and PYD domains-containing protein 1 OS=Homo sapiens GN=NLRP1 PE=1 SV=1 - [NALP1_HUMAN]
P59046	NACHT, LRR and PYD domains-containing protein 12 OS=Homo sapiens GN=NLRP12 PE=1 SV=2 - [NAL12_HUMAN]
Q86W24	NACHT, LRR and PYD domains-containing protein 14 OS=Homo sapiens GN=NLRP14 PE=1 SV=1 - [NAL14_HUMAN]
P59047	NACHT, LRR and PYD domains-containing protein 5 OS=Homo sapiens GN=NLRP5 PE=2 SV=2 - [NALP5_HUMAN]
Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]
Q8IXJ6	NAD-dependent protein deacetylase sirtuin-2 OS=Homo sapiens GN=SIRT2 PE=1 SV=2 - [SIR2_HUMAN]
Q9Y6E7	NAD-dependent protein lipoamidase sirtuin-4, mitochondrial OS=Homo sapiens GN=SIRT4 PE=1 SV=1 - [SIR4_HUMAN]
O43674	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Homo sapiens GN=NDUFB5 PE=1 SV=1 - [NDUB5_HUMAN]
O95139	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens GN=NDUFB6 PE=1 SV=3 - [NDUB6_HUMAN]
Q7L592	NADH dehydrogenase [ubiquinone] complex I, assembly factor 7 OS=Homo sapiens GN=NDUFAF7 PE=1 SV=1 - [NDUF7_HUMAN]
O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Homo sapiens GN=NDUFS4 PE=1 SV=1 - [NDUS4_HUMAN]
Q9UHQ9	NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1 - [NB5R1_HUMAN]
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3 - [NDUS1_HUMAN]
P03905	NADH-ubiquinone oxidoreductase chain 4 OS=Homo sapiens GN=MT-ND4 PE=1 SV=1 - [NU4M_HUMAN]
P03915	NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens GN=MT-ND5 PE=1 SV=2 - [NU5M_HUMAN]
Q16798	NADP-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME3 PE=2 SV=2 - [MAON_HUMAN]
Q6NXP6	NADP-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=NOXRED1 PE=2 SV=2 - [NXRD1_HUMAN]
Q9Y5S8	NADPH oxidase 1 OS=Homo sapiens GN=NOX1 PE=1 SV=2 - [NOX1_HUMAN]
Q6N069	N-alpha-acetyltransferase 16, NatA auxiliary subunit OS=Homo sapiens GN=NAA16 PE=1 SV=2 - [NAA16_HUMAN]
P61599	N-alpha-acetyltransferase 20 OS=Homo sapiens GN=NAA20 PE=1 SV=1 - [NAA20_HUMAN]
Q86UY6	N-alpha-acetyltransferase 40 OS=Homo sapiens GN=NAA40 PE=1 SV=1 - [NAA40_HUMAN]
Q6T4R5	Nance-Horan syndrome protein OS=Homo sapiens GN=NHS PE=1 SV=2 - [NHS_HUMAN]
Q14330	N-arachidonyl glycine receptor OS=Homo sapiens GN=GPR18 PE=2 SV=2 - [GPR18_HUMAN]
E9PAV3	Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1 - [NACAM_HUMAN]
O14513	Nck-associated protein 5 OS=Homo sapiens GN=NCKAP5 PE=1 SV=2 - [NCKP5_HUMAN]
Q9HCH0	Nck-associated protein 5-like OS=Homo sapiens GN=NCKAP5L PE=1 SV=2 - [NCK5L_HUMAN]
P20929	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=5 - [NEBU_HUMAN]
Q86VF7	Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2 - [NRAP_HUMAN]
Q9NQS3	Nectin-3 OS=Homo sapiens GN=PVRL3 PE=1 SV=1 - [PVRL3_HUMAN]
Q86UW6	NEDD4-binding protein 2 OS=Homo sapiens GN=N4BP2 PE=1 SV=2 - [N4BP2_HUMAN]
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2 OS=Homo sapiens GN=WWP2 PE=1 SV=2 - [WWP2_HUMAN]
Q9Y5A7	NEDD8 ultimate buster 1 OS=Homo sapiens GN=NUB1 PE=1 SV=2 - [NUB1_HUMAN]
Q9BU70	Nef-associated protein 1 OS=Homo sapiens GN=C9orf156 PE=1 SV=2 - [NAP1_HUMAN]
P18615	Negative elongation factor E OS=Homo sapiens GN=NELFE PE=1 SV=3 - [NELFE_HUMAN]
Q86YC3	Negative regulator of reactive oxygen species OS=Homo sapiens GN=NRROS PE=1 SV=1 - [NRROS_HUMAN]
O60500	Nephrin OS=Homo sapiens GN=NPHS1 PE=1 SV=1 - [NPHN_HUMAN]
Q7Z494	Nephrocystin-3 OS=Homo sapiens GN=NPHP3 PE=1 SV=1 - [NPHP3_HUMAN]

Q8NF91	Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=4 - [SYNE1_HUMAN]
Q8WXH0	Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3 - [SYNE2_HUMAN]
Q6ZMZ3	Nesprin-3 OS=Homo sapiens GN=SYNE3 PE=1 SV=2 - [SYNE3_HUMAN]
P48681	Nestin OS=Homo sapiens GN=NES PE=1 SV=2 - [NEST_HUMAN]
Q6ZN44	Netrin receptor UNC5A OS=Homo sapiens GN=UNC5A PE=1 SV=3 - [UNC5A_HUMAN]
Q6UXZ4	Netrin receptor UNC5D OS=Homo sapiens GN=UNC5D PE=2 SV=1 - [UNC5D_HUMAN]
Q8WUJ1	Neuferricin OS=Homo sapiens GN=CYB5D2 PE=2 SV=1 - [NEUFC_HUMAN]
O15394	Neural cell adhesion molecule 2 OS=Homo sapiens GN=NCAM2 PE=1 SV=2 - [NCAM2_HUMAN]
Q8NFP9	Neurobeachin OS=Homo sapiens GN=NBEA PE=1 SV=3 - [NBEA_HUMAN]
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]
A2RRP1	Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2 - [NBAS_HUMAN]
P07196	Neurofilament light polypeptide OS=Homo sapiens GN=NEFL PE=1 SV=3 - [NFL_HUMAN]
P07197	Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=3 - [NFM_HUMAN]
Q99466	Neurogenic locus notch homolog protein 4 OS=Homo sapiens GN=NOTCH4 PE=1 SV=2 - [NOTC4_HUMAN]
Q9BYT8	Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1 - [NEUL_HUMAN]
P28336	Neuromedin-B receptor OS=Homo sapiens GN=NMBR PE=1 SV=2 - [NMBR_HUMAN]
Q9GZQ4	Neuromedin-U receptor 2 OS=Homo sapiens GN=NMUR2 PE=1 SV=2 - [NMUR2_HUMAN]
Q8NEY1	Neuron navigator 1 OS=Homo sapiens GN=NAV1 PE=1 SV=2 - [NAV1_HUMAN]
Q8IVL1	Neuron navigator 2 OS=Homo sapiens GN=NAV2 PE=1 SV=3 - [NAV2_HUMAN]
Q9Y5X5	Neuropeptide FF receptor 2 OS=Homo sapiens GN=NPFFR2 PE=1 SV=2 - [NPFF2_HUMAN]
Q8TDF5	Neuropilin and tolloid-like protein 1 OS=Homo sapiens GN=NETO1 PE=2 SV=2 - [NETO1_HUMAN]
P43007	Neutral amino acid transporter A OS=Homo sapiens GN=SLC1A4 PE=1 SV=1 - [SATT_HUMAN]
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3 - [NCEH1_HUMAN]
P59665	Neutrophil defensin 1 OS=Homo sapiens GN=DEFA1 PE=1 SV=1 - [DEF1_HUMAN]
Q8NI38	NF-kappa-B inhibitor delta OS=Homo sapiens GN=NFKBID PE=1 SV=1 - [IKBD_HUMAN]
Q8N5F7	NF-kappa-B-activating protein OS=Homo sapiens GN=NKAP PE=1 SV=1 - [NKAP_HUMAN]
Q96TA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]
Q86XR2	Niban-like protein 2 OS=Homo sapiens GN=FAM129C PE=1 SV=2 - [NIBL2_HUMAN]
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1 - [NAMPT_HUMAN]
Q9HAN9	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1 OS=Homo sapiens GN=NMNAT1 PE=1 SV=1 - [NMNA1_HUMAN]
Q14112	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=3 - [NID2_HUMAN]
Q7Z2Y5	Nik-related protein kinase OS=Homo sapiens GN=NRK PE=1 SV=2 - [NRK_HUMAN]
Q9Y2I6	Ninein-like protein OS=Homo sapiens GN=NINL PE=1 SV=2 - [NINL_HUMAN]
Q9H841	NIPA-like protein 2 OS=Homo sapiens GN=NIPAL2 PE=2 SV=1 - [NPAL2_HUMAN]
Q9Y2I1	Nischarin OS=Homo sapiens GN=NISCH PE=1 SV=3 - [NISCH_HUMAN]
P29475	Nitric oxide synthase, brain OS=Homo sapiens GN=NOS1 PE=1 SV=2 - [NOS1_HUMAN]
P29474	Nitric oxide synthase, endothelial OS=Homo sapiens GN=NOS3 PE=1 SV=3 - [NOS3_HUMAN]
Q12980	Nitrogen permease regulator 3-like protein OS=Homo sapiens GN=NPRL3 PE=1 SV=1 - [NPRL3_HUMAN]
P30414	NK-tumor recognition protein OS=Homo sapiens GN=NKTR PE=1 SV=2 - [NKTR_HUMAN]
Q9NPP4	NLR family CARD domain-containing protein 4 OS=Homo sapiens GN=NLRC4 PE=1 SV=2 - [NLRC4_HUMAN]
Q9NRG4	N-lysine methyltransferase SMYD2 OS=Homo sapiens GN=SMYD2 PE=1 SV=2 - [SMYD2_HUMAN]
Q8NDF8	Non-canonical poly(A) RNA polymerase PAPD5 OS=Homo sapiens GN=PAPD5 PE=1 SV=2 - [PAPD5_HUMAN]
Q8IVI9	Nostrin OS=Homo sapiens GN=NOSTRIN PE=1 SV=2 - [NOSTN_HUMAN]
O60285	NUAK family SNF1-like kinase 1 OS=Homo sapiens GN=NUAK1 PE=1 SV=1 - [NUAK1_HUMAN]
P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 - [NASP_HUMAN]
Q8N9A8	Nuclear envelope phosphatase-regulatory subunit 1 OS=Homo sapiens GN=CNEP1R1 PE=1 SV=1 - [NEPR1_HUMAN]
Q00653	Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4 - [NFKB2_HUMAN]
P19838	Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens GN=NFKB1 PE=1 SV=2 - [NFKB1_HUMAN]
Q6P4R8	Nuclear factor related to kappa-B-binding protein OS=Homo sapiens GN=NFRKB PE=1 SV=2 - [NFRKB_HUMAN]
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 -

	[NUFP2_HUMAN]
P57740	Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1 - [NU107_HUMAN]
O75694	Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 - [NU155_HUMAN]
Q12769	Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 - [NU160_HUMAN]
P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 - [NU214_HUMAN]
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]
Q5VU65	Nuclear pore membrane glycoprotein 210-like OS=Homo sapiens GN=NUP210L PE=2 SV=1 - [P210L_HUMAN]
Q9HCD5	Nuclear receptor coactivator 5 OS=Homo sapiens GN=NCOA5 PE=1 SV=2 - [NCOA5_HUMAN]
Q9Y618	Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2 PE=1 SV=2 - [NCOR2_HUMAN]
P20393	Nuclear receptor subfamily 1 group D member 1 OS=Homo sapiens GN=NR1D1 PE=1 SV=1 - [NR1D1_HUMAN]
P22736	Nuclear receptor subfamily 4 group A member 1 OS=Homo sapiens GN=NR4A1 PE=1 SV=1 - [NR4A1_HUMAN]
Q15406	Nuclear receptor subfamily 6 group A member 1 OS=Homo sapiens GN=NR6A1 PE=1 SV=2 - [NR6A1_HUMAN]
Q9NSY0	Nuclear receptor-binding protein 2 OS=Homo sapiens GN=NRBP2 PE=2 SV=2 - [NRBP2_HUMAN]
P48552	Nuclear receptor-interacting protein 1 OS=Homo sapiens GN=NRIP1 PE=1 SV=2 - [NRIP1_HUMAN]
Q13823	Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 - [NOG2_HUMAN]
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1 - [NOM1_HUMAN]
O60287	Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4 - [NPA1P_HUMAN]
Q9H8H0	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 - [NOL11_HUMAN]
P78316	Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3 - [NOP14_HUMAN]
Q76FK4	Nucleolar protein 8 OS=Homo sapiens GN=NOL8 PE=1 SV=1 - [NOL8_HUMAN]
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]
Q5SRE5	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 - [NU188_HUMAN]
P12270	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]
A8MXV4	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial OS=Homo sapiens GN=NUDT19 PE=1 SV=1 - [NUD19_HUMAN]
Q12830	Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 - [BPTF_HUMAN]
Q5VT03	NUT family member 2D OS=Homo sapiens GN=NUTM2D PE=3 SV=2 - [NTM2D_HUMAN]
Q6UWF7	NXPE family member 4 OS=Homo sapiens GN=NXPE4 PE=2 SV=1 - [NXPE4_HUMAN]
Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2 - [MACD1_HUMAN]
Q5VST9	Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3 - [OBSCN_HUMAN]
Q6UWY5	Olfactomedin-like protein 1 OS=Homo sapiens GN=OLFML1 PE=1 SV=2 - [OLFL1_HUMAN]
Q6IF99	Olfactory receptor 10K2 OS=Homo sapiens GN=OR10K2 PE=3 SV=1 - [O10K2_HUMAN]
Q8NGN2	Olfactory receptor 10S1 OS=Homo sapiens GN=OR10S1 PE=2 SV=2 - [O10S1_HUMAN]
Q8NGY1	Olfactory receptor 10Z1 OS=Homo sapiens GN=OR10Z1 PE=3 SV=1 - [O10Z1_HUMAN]
Q8NGC8	Olfactory receptor 11H7 OS=Homo sapiens GN=OR11H7 PE=3 SV=2 - [O11H7_HUMAN]
Q9UGF7	Olfactory receptor 12D3 OS=Homo sapiens GN=OR12D3 PE=2 SV=1 - [O12D3_HUMAN]
Q96R54	Olfactory receptor 14A2 OS=Homo sapiens GN=OR14A2 PE=3 SV=2 - [O14A2_HUMAN]
Q8WZA6	Olfactory receptor 1E3 OS=Homo sapiens GN=OR1E3 PE=3 SV=2 - [OR1E3_HUMAN]
Q8NGE2	Olfactory receptor 2AP1 OS=Homo sapiens GN=OR2AP1 PE=3 SV=1 - [O2AP1_HUMAN]
Q8NGZ4	Olfactory receptor 2G3 OS=Homo sapiens GN=OR2G3 PE=2 SV=1 - [OR2G3_HUMAN]
O43869	Olfactory receptor 2T1 OS=Homo sapiens GN=OR2T1 PE=3 SV=3 - [OR2T1_HUMAN]
P58180	Olfactory receptor 4D2 OS=Homo sapiens GN=OR4D2 PE=2 SV=1 - [OR4D2_HUMAN]
Q8NGJ6	Olfactory receptor 51A4 OS=Homo sapiens GN=OR51A4 PE=3 SV=1 - [O51A4_HUMAN]
Q9H340	Olfactory receptor 51B6 OS=Homo sapiens GN=OR51B6 PE=3 SV=2 - [O51B6_HUMAN]
Q9H255	Olfactory receptor 51E2 OS=Homo sapiens GN=OR51E2 PE=2 SV=1 - [O51E2_HUMAN]
Q8NGJ5	Olfactory receptor 51L1 OS=Homo sapiens GN=OR51L1 PE=3 SV=1 - [O51L1_HUMAN]
Q9H2C8	Olfactory receptor 51V1 OS=Homo sapiens GN=OR51V1 PE=3 SV=2 - [O51V1_HUMAN]
Q96RD2	Olfactory receptor 52B2 OS=Homo sapiens GN=OR52B2 PE=2 SV=3 - [O52B2_HUMAN]
Q8NGK2	Olfactory receptor 52B4 OS=Homo sapiens GN=OR52B4 PE=3 SV=2 - [O52B4_HUMAN]
Q8NGI2	Olfactory receptor 52N4 OS=Homo sapiens GN=OR52N4 PE=2 SV=2 - [O52N4_HUMAN]

Q8NH54	Olfactory receptor 56A3 OS=Homo sapiens GN=OR56A3 PE=3 SV=2 - [O56A3_HUMAN]
Q8NGL1	Olfactory receptor 5D18 OS=Homo sapiens GN=OR5D18 PE=2 SV=1 - [OR5DI_HUMAN]
Q8NGV7	Olfactory receptor 5H2 OS=Homo sapiens GN=OR5H2 PE=3 SV=3 - [OR5H2_HUMAN]
Q96RA2	Olfactory receptor 7D2 OS=Homo sapiens GN=OR7D2 PE=2 SV=2 - [OR7D2_HUMAN]
Q8NGQ6	Olfactory receptor 9I1 OS=Homo sapiens GN=OR9I1 PE=3 SV=1 - [OR9I1_HUMAN]
Q8TAK6	Oligodendrocyte transcription factor 1 OS=Homo sapiens GN=OLIG1 PE=1 SV=2 - [OLIG1_HUMAN]
Q6U736	Opsin-5 OS=Homo sapiens GN=OPN5 PE=1 SV=3 - [OPN5_HUMAN]
Q96CV9	Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 - [OPTN_HUMAN]
O75665	Oral-facial-digital syndrome 1 protein OS=Homo sapiens GN=OFD1 PE=1 SV=1 - [OFD1_HUMAN]
O43613	Orexin receptor type 1 OS=Homo sapiens GN=HCRTR1 PE=2 SV=2 - [OX1R_HUMAN]
P11926	Ornithine decarboxylase OS=Homo sapiens GN=ODC1 PE=1 SV=2 - [DCOR_HUMAN]
Q9HC10	Otoferlin OS=Homo sapiens GN=OTOF PE=1 SV=3 - [OTOF_HUMAN]
Q8TE49	OTU domain-containing protein 7A OS=Homo sapiens GN=OTUD7A PE=1 SV=1 - [OTU7A_HUMAN]
Q9NX31	Oxidative stress-responsive serine-rich protein 1 OS=Homo sapiens GN=OSER1 PE=2 SV=2 - [OSER1_HUMAN]
P56715	Oxygen-regulated protein 1 OS=Homo sapiens GN=RP1 PE=1 SV=1 - [RP1_HUMAN]
P30559	Oxytocin receptor OS=Homo sapiens GN=OXTR PE=2 SV=2 - [OXYR_HUMAN]
Q04671	P protein OS=Homo sapiens GN=OCA2 PE=1 SV=2 - [P_HUMAN]
Q9UBL9	P2X purinoceptor 2 OS=Homo sapiens GN=P2RX2 PE=1 SV=1 - [P2RX2_HUMAN]
Q93086	P2X purinoceptor 5 OS=Homo sapiens GN=P2RX5 PE=2 SV=4 - [P2RX5_HUMAN]
Q58A45	PAB-dependent poly(A)-specific ribonuclease subunit PAN3 OS=Homo sapiens GN=PAN3 PE=1 SV=3 - [PAN3_HUMAN]
O75182	Paired amphipathic helix protein Sin3b OS=Homo sapiens GN=SIN3B PE=1 SV=2 - [SIN3B_HUMAN]
O43316	Paired box protein Pax-4 OS=Homo sapiens GN=PAX4 PE=1 SV=1 - [PAX4_HUMAN]
P23759	Paired box protein Pax-7 OS=Homo sapiens GN=PAX7 PE=1 SV=4 - [PAX7_HUMAN]
Q9C0B5	Palmitoyltransferase ZDHHC5 OS=Homo sapiens GN=ZDHHC5 PE=1 SV=2 - [ZDHC5_HUMAN]
P20962	Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2 - [PTMS_HUMAN]
P01270	Parathyroid hormone OS=Homo sapiens GN=PTH PE=1 SV=1 - [PTHY_HUMAN]
Q8TEW8	Partitioning defective 3 homolog B OS=Homo sapiens GN=PARD3B PE=1 SV=2 - [PAR3L_HUMAN]
Q8TEW0	Partitioning defective 3 homolog OS=Homo sapiens GN=PARD3 PE=1 SV=2 - [PARD3_HUMAN]
Q8N8W4	Patatin-like phospholipase domain-containing protein 1 OS=Homo sapiens GN=PNPLA1 PE=1 SV=3 - [PLPL1_HUMAN]
Q9NWS1	PCNA-interacting partner OS=Homo sapiens GN=PARPBP PE=1 SV=3 - [PARI_HUMAN]
O15018	PDZ domain-containing protein 2 OS=Homo sapiens GN=PDZD2 PE=1 SV=4 - [PDZD2_HUMAN]
Q76G19	PDZ domain-containing protein 4 OS=Homo sapiens GN=PDZD4 PE=1 SV=1 - [PDZD4_HUMAN]
Q8NEN9	PDZ domain-containing protein 8 OS=Homo sapiens GN=PDZD8 PE=1 SV=1 - [PDZD8_HUMAN]
Q8TF65	PDZ domain-containing protein GIPC2 OS=Homo sapiens GN=GIPC2 PE=1 SV=1 - [GIPC2_HUMAN]
Q6ZMN7	PDZ domain-containing RING finger protein 4 OS=Homo sapiens GN=PDZRN4 PE=2 SV=3 - [PZRN4_HUMAN]
Q96RV3	Pecanex-like protein 1 OS=Homo sapiens GN=PCNX PE=1 SV=2 - [PCX1_HUMAN]
Q9H6A9	Pecanex-like protein 3 OS=Homo sapiens GN=PCNXL3 PE=1 SV=2 - [PCX3_HUMAN]
O43511	Pendrin OS=Homo sapiens GN=SLC26A4 PE=1 SV=1 - [S26A4_HUMAN]
Q9UGC7	Peptide chain release factor 1-like, mitochondrial OS=Homo sapiens GN=MTRF1L PE=1 SV=1 - [RF1ML_HUMAN]
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2 - [PPIA_HUMAN]
Q9Y680	Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Homo sapiens GN=FKBP7 PE=1 SV=1 - [FKBP7_HUMAN]
Q13427	Peptidyl-prolyl cis-trans isomerase G OS=Homo sapiens GN=PPIG PE=1 SV=2 - [PPIG_HUMAN]
P55201	Peregrin OS=Homo sapiens GN=BRPF1 PE=1 SV=2 - [BRPF1_HUMAN]
O95613	Pericentrin OS=Homo sapiens GN=PCNT PE=1 SV=4 - [PCNT_HUMAN]
Q15154	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 - [PCM1_HUMAN]
Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]
O14936	Peripheral plasma membrane protein CASK OS=Homo sapiens GN=CASK PE=1 SV=3 - [CSKP_HUMAN]
O95153	Peripheral-type benzodiazepine receptor-associated protein 1 OS=Homo sapiens GN=BZRAP1 PE=1 SV=2 - [RIMB1_HUMAN]
O60437	Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4 - [PEPL_HUMAN]
A1KZ92	Peroxidasin-like protein OS=Homo sapiens GN=PXDNL PE=1 SV=3 - [PXDNL_HUMAN]

P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]
O75192	Peroxisomal membrane protein 11A OS=Homo sapiens GN=PEX11A PE=1 SV=1 - [PX11A_HUMAN]
Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=1 SV=2 - [SOX_HUMAN]
O43933	Peroxisome biogenesis factor 1 OS=Homo sapiens GN=PEX1 PE=1 SV=1 - [PEX1_HUMAN]
O60683	Peroxisome biogenesis factor 10 OS=Homo sapiens GN=PEX10 PE=1 SV=1 - [PEX10_HUMAN]
Q86YN6	Peroxisome proliferator-activated receptor gamma coactivator 1-beta OS=Homo sapiens GN=PPARGC1B PE=1 SV=2 - [PRGC2_HUMAN]
P37231	Peroxisome proliferator-activated receptor gamma OS=Homo sapiens GN=PPARG PE=1 SV=3 - [PPARG_HUMAN]
Q9H720	PGAP2-interacting protein OS=Homo sapiens GN=CWH43 PE=2 SV=2 - [PG2IP_HUMAN]
Q9NYI0	PH and SEC7 domain-containing protein 3 OS=Homo sapiens GN=PSD3 PE=1 SV=2 - [PSD3_HUMAN]
O43189	PHD finger protein 1 OS=Homo sapiens GN=PHF1 PE=1 SV=3 - [PHF1_HUMAN]
Q96QT6	PHD finger protein 12 OS=Homo sapiens GN=PHF12 PE=1 SV=2 - [PHF12_HUMAN]
O94880	PHD finger protein 14 OS=Homo sapiens GN=PHF14 PE=1 SV=2 - [PHF14_HUMAN]
Q96EK2	PHD finger protein 21B OS=Homo sapiens GN=PHF21B PE=2 SV=1 - [PF21B_HUMAN]
Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]
Q8WWQ0	PH-interacting protein OS=Homo sapiens GN=PHIP PE=1 SV=2 - [PHIP_HUMAN]
Q5VZY2	Phosphatidate phosphatase PPAPDC1A OS=Homo sapiens GN=PPAPDC1A PE=1 SV=2 - [PPC1A_HUMAN]
Q9Y2H2	Phosphatidylinositide phosphatase SAC2 OS=Homo sapiens GN=INPP5F PE=1 SV=3 - [SAC2_HUMAN]
Q6XPS3	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2 OS=Homo sapiens GN=TPTE2 PE=1 SV=2 - [TPTE2_HUMAN]
Q8TCU6	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein OS=Homo sapiens GN=PREX1 PE=1 SV=3 - [PREX1_HUMAN]
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1 - [P4K2A_HUMAN]
O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Homo sapiens GN=PIK3C2A PE=1 SV=2 - [P3C2A_HUMAN]
O00750	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta OS=Homo sapiens GN=PIK3C2B PE=1 SV=2 - [P3C2B_HUMAN]
O75747	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit gamma OS=Homo sapiens GN=PIK3C2G PE=1 SV=3 - [P3C2G_HUMAN]
Q92535	Phosphatidylinositol N-acetylglucosaminyltransferase subunit C OS=Homo sapiens GN=PIGC PE=2 SV=1 - [PIGC_HUMAN]
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2 - [PICAL_HUMAN]
Q7Z7B1	Phosphatidylinositol-glycan biosynthesis class W protein OS=Homo sapiens GN=PIGW PE=1 SV=1 - [PIGW_HUMAN]
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]
Q96G03	Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4 - [PGM2_HUMAN]
Q15124	Phosphoglucomutase-like protein 5 OS=Homo sapiens GN=PGM5 PE=1 SV=2 - [PGM5_HUMAN]
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]
Q6ZUJ8	Phosphoinositide 3-kinase adapter protein 1 OS=Homo sapiens GN=PIK3AP1 PE=1 SV=2 - [BCAP_HUMAN]
Q99570	Phosphoinositide 3-kinase regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=1 SV=3 - [PI3R4_HUMAN]
Q5UE93	Phosphoinositide 3-kinase regulatory subunit 6 OS=Homo sapiens GN=PIK3R6 PE=1 SV=1 - [PI3R6_HUMAN]
Q8WU67	Phospholipase ABHD3 OS=Homo sapiens GN=ABHD3 PE=1 SV=2 - [ABHD3_HUMAN]
Q6P1J6	Phospholipase B1, membrane-associated OS=Homo sapiens GN=PLB1 PE=1 SV=3 - [PLB1_HUMAN]
P55058	Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1 - [PLTP_HUMAN]
O43520	Phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3 - [AT8B1_HUMAN]
P98198	Phospholipid-transporting ATPase ID OS=Homo sapiens GN=ATP8B2 PE=1 SV=2 - [AT8B2_HUMAN]
Q8NB49	Phospholipid-transporting ATPase IG OS=Homo sapiens GN=ATP11C PE=1 SV=3 - [AT11C_HUMAN]
O15305	Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=1 SV=1 - [PMM2_HUMAN]
Q9HAB8	Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2 - [PPCS_HUMAN]
O60256	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1 - [KPRB_HUMAN]
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMAN]
P46019	Phosphorylase b kinase regulatory subunit alpha, liver isoform OS=Homo sapiens GN=PHKA2 PE=1 SV=1 - [KPB2_HUMAN]
Q93100	Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3 - [KPBB_HUMAN]
Q6NYC8	Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 - [PPR18_HUMAN]

Q9H5I5	Piezo-type mechanosensitive ion channel component 2 OS=Homo sapiens GN=PIEZO2 PE=1 SV=2 - [PIEZ2_HUMAN]
Q8WWB5	PIH1 domain-containing protein 2 OS=Homo sapiens GN=PIH1D2 PE=1 SV=1 - [PIHD2_HUMAN]
Q63HQ2	Pikachurin OS=Homo sapiens GN=EGFLAM PE=1 SV=2 - [EGFLA_HUMAN]
O75364	Pituitary homeobox 3 OS=Homo sapiens GN=PITX3 PE=1 SV=1 - [PITX3_HUMAN]
P28069	Pituitary-specific positive transcription factor 1 OS=Homo sapiens GN=POU1F1 PE=1 SV=1 - [PIT1_HUMAN]
Q7Z3Z3	Piwi-like protein 3 OS=Homo sapiens GN=PIWIL3 PE=2 SV=2 - [PIWL3_HUMAN]
Q7Z3Z4	Piwi-like protein 4 OS=Homo sapiens GN=PIWIL4 PE=2 SV=2 - [PIWL4_HUMAN]
Q99959	Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 - [PKP2_HUMAN]
P20020	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3 - [AT2B1_HUMAN]
P05155	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2 - [IC1_HUMAN]
P13797	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 - [PLST_HUMAN]
P16284	Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1 - [PECA1_HUMAN]
Q9HB19	Pleckstrin homology domain-containing family A member 2 OS=Homo sapiens GN=PLEKHA2 PE=1 SV=2 - [PKHA2_HUMAN]
Q9H7P9	Pleckstrin homology domain-containing family G member 2 OS=Homo sapiens GN=PLEKHG2 PE=1 SV=3 - [PKHG2_HUMAN]
Q96PX9	Pleckstrin homology domain-containing family G member 4B OS=Homo sapiens GN=PLEKHG4B PE=2 SV=4 - [PKH4B_HUMAN]
Q7Z736	Pleckstrin homology domain-containing family H member 3 OS=Homo sapiens GN=PLEKHH3 PE=1 SV=2 - [PKHH3_HUMAN]
Q6ZWE6	Pleckstrin homology domain-containing family M member 3 OS=Homo sapiens GN=PLEKHM3 PE=2 SV=2 - [PKHM3_HUMAN]
Q86UU1	Pleckstrin homology-like domain family B member 1 OS=Homo sapiens GN=PHLDB1 PE=1 SV=1 - [PHLB1_HUMAN]
Q86SQ0	Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2 PE=1 SV=2 - [PHLB2_HUMAN]
Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]
O75051	Plexin-A2 OS=Homo sapiens GN=PLXNA2 PE=1 SV=4 - [PLXA2_HUMAN]
O60486	Plexin-C1 OS=Homo sapiens GN=PLXNC1 PE=1 SV=1 - [PLXC1_HUMAN]
Q8NBT0	POC1 centriolar protein homolog A OS=Homo sapiens GN=POC1A PE=1 SV=2 - [POC1A_HUMAN]
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]
Q460N3	Poly [ADP-ribose] polymerase 15 OS=Homo sapiens GN=PARP15 PE=1 SV=2 - [PAR15_HUMAN]
Q9BWT3	Poly(A) polymerase gamma OS=Homo sapiens GN=PAPOLG PE=1 SV=2 - [PAPOG_HUMAN]
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]
Q9UHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [PUF60_HUMAN]
Q9H361	Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2 - [PABP3_HUMAN]
Q96GD3	Polycomb protein SCMH1 OS=Homo sapiens GN=SCMH1 PE=1 SV=1 - [SCMH1_HUMAN]
Q9NTG1	Polycystic kidney disease and receptor for egg jelly-related protein OS=Homo sapiens GN=PKDREJ PE=2 SV=2 - [PKDRE_HUMAN]
Q7Z443	Polycystic kidney disease protein 1-like 3 OS=Homo sapiens GN=PKD1L3 PE=1 SV=1 - [PK1L3_HUMAN]
P98161	Polycystin-1 OS=Homo sapiens GN=PKD1 PE=1 SV=3 - [PKD1_HUMAN]
Q13563	Polycystin-2 OS=Homo sapiens GN=PKD2 PE=1 SV=3 - [PKD2_HUMAN]
Q8IXK0	Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 - [PHC2_HUMAN]
Q8IXK2	Polypeptide N-acetylgalactosaminyltransferase 12 OS=Homo sapiens GN=GALNT12 PE=1 SV=3 - [GLT12_HUMAN]
Q8NCL4	Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2 - [GALT6_HUMAN]
Q49A17	Polypeptide N-acetylgalactosaminyltransferase-like 6 OS=Homo sapiens GN=GALNTL6 PE=2 SV=2 - [GLTL6_HUMAN]
Q9UKA9	Polypyrimidine tract-binding protein 2 OS=Homo sapiens GN=PTBP2 PE=1 SV=1 - [PTBP2_HUMAN]
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]
Q96KW2	POM121-like protein 2 OS=Homo sapiens GN=POM121L2 PE=3 SV=2 - [P12L2_HUMAN]
P57789	Potassium channel subfamily K member 10 OS=Homo sapiens GN=KCNK10 PE=1 SV=1 - [KCNKA_HUMAN]
Q96T55	Potassium channel subfamily K member 16 OS=Homo sapiens GN=KCNK16 PE=1 SV=1 - [KCNKG_HUMAN]
O95279	Potassium channel subfamily K member 5 OS=Homo sapiens GN=KCNK5 PE=1 SV=1 - [KCNK5_HUMAN]
A8MYU2	Potassium channel subfamily U member 1 OS=Homo sapiens GN=KCNU1 PE=1 SV=2 - [KCNU1_HUMAN]
Q14721	Potassium voltage-gated channel subfamily B member 1 OS=Homo sapiens GN=KCNB1 PE=1 SV=2 - [KCNB1_HUMAN]

Q03721	Potassium voltage-gated channel subfamily C member 4 OS=Homo sapiens GN=KCNC4 PE=1 SV=2 - [KCNC4_HUMAN]
Q8TDN1	Potassium voltage-gated channel subfamily G member 4 OS=Homo sapiens GN=KCNG4 PE=1 SV=1 - [KCNG4_HUMAN]
O95259	Potassium voltage-gated channel subfamily H member 1 OS=Homo sapiens GN=KCNH1 PE=1 SV=1 - [KCNH1_HUMAN]
Q96L42	Potassium voltage-gated channel subfamily H member 8 OS=Homo sapiens GN=KCNH8 PE=2 SV=2 - [KCNH8_HUMAN]
P51787	Potassium voltage-gated channel subfamily KQT member 1 OS=Homo sapiens GN=KCNQ1 PE=1 SV=3 - [KCNQ1_HUMAN]
Q9Y3Q4	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4 OS=Homo sapiens GN=HCN4 PE=1 SV=1 - [HCN4_HUMAN]
Q01860	POU domain, class 5, transcription factor 1 OS=Homo sapiens GN=POU5F1 PE=1 SV=1 - [PO5F1_HUMAN]
Q14863	POU domain, class 6, transcription factor 1 OS=Homo sapiens GN=POU6F1 PE=1 SV=1 - [PO6F1_HUMAN]
Q9H4Q3	PR domain zinc finger protein 13 OS=Homo sapiens GN=PRDM13 PE=2 SV=2 - [PRD13_HUMAN]
Q9GZV8	PR domain zinc finger protein 14 OS=Homo sapiens GN=PRDM14 PE=1 SV=1 - [PRD14_HUMAN]
Q13029	PR domain zinc finger protein 2 OS=Homo sapiens GN=PRDM2 PE=1 SV=3 - [PRDM2_HUMAN]
P40425	Pre-B-cell leukemia transcription factor 2 OS=Homo sapiens GN=PBX2 PE=1 SV=2 - [PBX2_HUMAN]
P20742	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4 - [PZP_HUMAN]
Q86UA1	Pre-mRNA-processing factor 39 OS=Homo sapiens GN=PRPF39 PE=1 SV=3 - [PRP39_HUMAN]
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HUMAN]
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN]
Q9HCG8	Pre-mRNA-splicing factor CWC22 homolog OS=Homo sapiens GN=CWC22 PE=1 SV=3 - [CWC22_HUMAN]
Q9NXE8	Pre-mRNA-splicing factor CWC25 homolog OS=Homo sapiens GN=CWC25 PE=1 SV=1 - [CWC25_HUMAN]
Q15007	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2 - [FL2D_HUMAN]
Q5JRX3	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3 - [PREP_HUMAN]
O43900	Prickle-like protein 3 OS=Homo sapiens GN=PRICKLE3 PE=1 SV=2 - [PRIC3_HUMAN]
Q6NUJ1	Proactivator polypeptide-like 1 OS=Homo sapiens GN=PSAPL1 PE=2 SV=2 - [SAPL1_HUMAN]
A2PYH4	Probable ATP-dependent DNA helicase HFM1 OS=Homo sapiens GN=HFM1 PE=1 SV=2 - [HFM1_HUMAN]
Q13206	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens GN=DDX10 PE=1 SV=2 - [DDX10_HUMAN]
Q9UJV9	Probable ATP-dependent RNA helicase DDX41 OS=Homo sapiens GN=DDX41 PE=1 SV=2 - [DDX41_HUMAN]
Q9NXZ2	Probable ATP-dependent RNA helicase DDX43 OS=Homo sapiens GN=DDX43 PE=2 SV=2 - [DDX43_HUMAN]
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_HUMAN]
O95786	Probable ATP-dependent RNA helicase DDX58 OS=Homo sapiens GN=DDX58 PE=1 SV=2 - [DDX58_HUMAN]
Q5T1V6	Probable ATP-dependent RNA helicase DDX59 OS=Homo sapiens GN=DDX59 PE=1 SV=1 - [DDX59_HUMAN]
Q8IY21	Probable ATP-dependent RNA helicase DDX60 OS=Homo sapiens GN=DDX60 PE=1 SV=3 - [DDX60_HUMAN]
Q9H7F0	Probable cation-transporting ATPase 13A3 OS=Homo sapiens GN=ATP13A3 PE=1 SV=4 - [AT133_HUMAN]
Q6NUT2	Probable C-mannosyltransferase DPY19L2 OS=Homo sapiens GN=DPY19L2 PE=1 SV=2 - [D19L2_HUMAN]
Q6ZPD9	Probable C-mannosyltransferase DPY19L3 OS=Homo sapiens GN=DPY19L3 PE=2 SV=1 - [D19L3_HUMAN]
Q9HA77	Probable cysteine--tRNA ligase, mitochondrial OS=Homo sapiens GN=CARS2 PE=1 SV=1 - [SYCM_HUMAN]
Q15751	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2 - [HERC1_HUMAN]
P28370	Probable global transcription activator SNF2L1 OS=Homo sapiens GN=SMARCA1 PE=1 SV=2 - [SMCA1_HUMAN]
Q7Z602	Probable G-protein coupled receptor 141 OS=Homo sapiens GN=GPR141 PE=2 SV=1 - [GP141_HUMAN]
Q96CH1	Probable G-protein coupled receptor 146 OS=Homo sapiens GN=GPR146 PE=2 SV=1 - [GP146_HUMAN]
Q86SP6	Probable G-protein coupled receptor 149 OS=Homo sapiens GN=GPR149 PE=2 SV=2 - [GP149_HUMAN]
Q5T848	Probable G-protein coupled receptor 158 OS=Homo sapiens GN=GPR158 PE=1 SV=1 - [GP158_HUMAN]
Q9UJ42	Probable G-protein coupled receptor 160 OS=Homo sapiens GN=GPR160 PE=2 SV=1 - [GP160_HUMAN]
Q6PRD1	Probable G-protein coupled receptor 179 OS=Homo sapiens GN=GPR179 PE=1 SV=2 - [GP179_HUMAN]
Q9BZJ8	Probable G-protein coupled receptor 61 OS=Homo sapiens GN=GPR61 PE=2 SV=2 - [GPR61_HUMAN]
Q9BZJ7	Probable G-protein coupled receptor 62 OS=Homo sapiens GN=GPR62 PE=2 SV=2 - [GPR62_HUMAN]
O95800	Probable G-protein coupled receptor 75 OS=Homo sapiens GN=GPR75 PE=1 SV=1 - [GPR75_HUMAN]
Q7Z333	Probable helicase senataxin OS=Homo sapiens GN=SETX PE=1 SV=4 - [SETX_HUMAN]

Q96NU7	Probable imidazolonepropionase OS=Homo sapiens GN=AMDHD1 PE=1 SV=2 - [HUTI_HUMAN]
Q13395	Probable methyltransferase TARBP1 OS=Homo sapiens GN=TARBP1 PE=1 SV=1 - [TARB1_HUMAN]
P0C7U3	Probable palmitoyltransferase ZDHHC11B OS=Homo sapiens GN=ZDHHC11B PE=3 SV=1 - [ZH11B_HUMAN]
Q8IZN3	Probable palmitoyltransferase ZDHHC14 OS=Homo sapiens GN=ZDHHC14 PE=1 SV=1 - [ZDH14_HUMAN]
Q9Y2G3	Probable phospholipid-transporting ATPase IF OS=Homo sapiens GN=ATP11B PE=1 SV=2 - [AT11B_HUMAN]
P98196	Probable phospholipid-transporting ATPase IH OS=Homo sapiens GN=ATP11A PE=1 SV=3 - [AT11A_HUMAN]
Q8WWH5	Probable tRNA pseudouridine synthase 1 OS=Homo sapiens GN=TRUB1 PE=1 SV=1 - [TRUB1_HUMAN]
O95900	Probable tRNA pseudouridine synthase 2 OS=Homo sapiens GN=TRUB2 PE=1 SV=1 - [TRUB2_HUMAN]
O95922	Probable tubulin polyglutamylase TTLL1 OS=Homo sapiens GN=TTLL1 PE=2 SV=1 - [TTLL1_HUMAN]
Q3SXZ7	Probable tubulin polyglutamylase TTLL9 OS=Homo sapiens GN=TTLL9 PE=2 SV=3 - [TTLL9_HUMAN]
P01133	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2 - [EGF_HUMAN]
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]
P06401	Progesterone receptor OS=Homo sapiens GN=PGR PE=1 SV=4 - [PRGR_HUMAN]
Q9BUL8	Programmed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1 - [PDC10_HUMAN]
Q53EL6	Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 PE=1 SV=2 - [PDCD4_HUMAN]
Q9HCJ1	Progressive ankylosis protein homolog OS=Homo sapiens GN=ANKH PE=1 SV=2 - [ANKH_HUMAN]
P35232	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 - [PHB_HUMAN]
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]
Q6PGN9	Proline/serine-rich coiled-coil protein 1 OS=Homo sapiens GN=PSRC1 PE=1 SV=1 - [PSRC1_HUMAN]
Q96B36	Proline-rich AKT1 substrate 1 OS=Homo sapiens GN=AKT1S1 PE=1 SV=1 - [AKTS1_HUMAN]
Q86XR5	Proline-rich membrane anchor 1 OS=Homo sapiens GN=PRIMA1 PE=1 SV=2 - [PRIMA_HUMAN]
Q96HE9	Proline-rich protein 11 OS=Homo sapiens GN=PRR11 PE=1 SV=1 - [PRR11_HUMAN]
Q9NZ81	Proline-rich protein 13 OS=Homo sapiens GN=PRR13 PE=1 SV=1 - [PRR13_HUMAN]
A6NEV1	Proline-rich protein 23A OS=Homo sapiens GN=PRR23A PE=3 SV=1 - [PR23A_HUMAN]
Q9H6K5	Proline-rich protein 36 OS=Homo sapiens GN=PRR36 PE=2 SV=2 - [PRR36_HUMAN]
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2 - [LRP1_HUMAN]
Q8IVL5	Prolyl 3-hydroxylase 2 OS=Homo sapiens GN=LEPREL1 PE=1 SV=1 - [P3H2_HUMAN]
P13674	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2 - [P4HA1_HUMAN]
O43490	Prominin-1 OS=Homo sapiens GN=PROM1 PE=1 SV=1 - [PROM1_HUMAN]
Q02297	Pro-neuregulin-1, membrane-bound isoform OS=Homo sapiens GN=NRG1 PE=1 SV=3 - [NRG1_HUMAN]
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]
Q8NBP7	Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN=PCSK9 PE=1 SV=3 - [PCSK9_HUMAN]
P04808	Prorelaxin H1 OS=Homo sapiens GN=RLN1 PE=2 SV=1 - [REL1_HUMAN]
O15354	Prosaposin receptor GPR37 OS=Homo sapiens GN=GPR37 PE=1 SV=2 - [GPR37_HUMAN]
Q9H7Z7	Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1 - [PGES2_HUMAN]
P43115	Prostaglandin E2 receptor EP3 subtype OS=Homo sapiens GN=PTGER3 PE=2 SV=1 - [PE2R3_HUMAN]
P35408	Prostaglandin E2 receptor EP4 subtype OS=Homo sapiens GN=PTGER4 PE=1 SV=1 - [PE2R4_HUMAN]
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2 - [ECM29_HUMAN]
P55198	Protein AF-17 OS=Homo sapiens GN=MLLT6 PE=1 SV=2 - [AF17_HUMAN]
Q8IVF2	Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNK2_HUMAN]
Q5T1N1	Protein AKNAD1 OS=Homo sapiens GN=AKNAD1 PE=2 SV=3 - [AKND1_HUMAN]
A6NFN9	Protein ANKUB1 OS=Homo sapiens GN=ANKUB1 PE=2 SV=2 - [ANKUB_HUMAN]
Q9HCK5	Protein argonaute-4 OS=Homo sapiens GN=AGO4 PE=1 SV=2 - [AGO4_HUMAN]
Q9UPA5	Protein bassoon OS=Homo sapiens GN=BSN PE=2 SV=4 - [BSN_HUMAN]
Q96NH3	Protein broad-minded OS=Homo sapiens GN=TBC1D32 PE=2 SV=4 - [BROMI_HUMAN]
Q8TCG1	Protein CIP2A OS=Homo sapiens GN=KIAA1524 PE=1 SV=2 - [CIP2A_HUMAN]
Q9UBY8	Protein CLN8 OS=Homo sapiens GN=CLN8 PE=1 SV=3 - [CLN8_HUMAN]
Q9P219	Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3 - [DAPLE_HUMAN]

Q9UBU7	Protein DBF4 homolog A OS=Homo sapiens GN=DBF4 PE=1 SV=1 - [DBF4A_HUMAN]
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1 - [DDI2_HUMAN]
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]
Q8NEG7	Protein DENND6B OS=Homo sapiens GN=DENND6B PE=2 SV=1 - [DEN6B_HUMAN]
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 - [DIAP1_HUMAN]
O60879	Protein diaphanous homolog 2 OS=Homo sapiens GN=DIAPH2 PE=1 SV=1 - [DIAP2_HUMAN]
Q13087	Protein disulfide-isomerase A2 OS=Homo sapiens GN=PDIA2 PE=1 SV=2 - [PDIA2_HUMAN]
Q14554	Protein disulfide-isomerase A5 OS=Homo sapiens GN=PDIA5 PE=1 SV=1 - [PDIA5_HUMAN]
Q9Y3R5	Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5 - [DOP2_HUMAN]
Q9NYP3	Protein downstream neighbor of Son OS=Homo sapiens GN=DONSON PE=1 SV=2 - [DONS_HUMAN]
Q14156	Protein EFR3 homolog A OS=Homo sapiens GN=EFR3A PE=1 SV=2 - [EFR3A_HUMAN]
Q9Y2G0	Protein EFR3 homolog B OS=Homo sapiens GN=EFR3B PE=1 SV=2 - [EFR3B_HUMAN]
Q03111	Protein ENL OS=Homo sapiens GN=MLLT1 PE=1 SV=2 - [ENL_HUMAN]
Q5T1H1	Protein eyes shut homolog OS=Homo sapiens GN=EYS PE=1 SV=5 - [EYS_HUMAN]
O95990	Protein FAM107A OS=Homo sapiens GN=FAM107A PE=1 SV=1 - [F107A_HUMAN]
Q9BPY3	Protein FAM118B OS=Homo sapiens GN=FAM118B PE=1 SV=1 - [F118B_HUMAN]
Q5BKY9	Protein FAM133B OS=Homo sapiens GN=FAM133B PE=1 SV=1 - [F133B_HUMAN]
O94988	Protein FAM13A OS=Homo sapiens GN=FAM13A PE=1 SV=2 - [FA13A_HUMAN]
A5PLN7	Protein FAM149A OS=Homo sapiens GN=FAM149A PE=2 SV=2 - [F149A_HUMAN]
Q5T6X4	Protein FAM162B OS=Homo sapiens GN=FAM162B PE=2 SV=1 - [F162B_HUMAN]
Q5VUB5	Protein FAM171A1 OS=Homo sapiens GN=FAM171A1 PE=1 SV=1 - [F1711_HUMAN]
A8MVW0	Protein FAM171A2 OS=Homo sapiens GN=FAM171A2 PE=1 SV=1 - [F1712_HUMAN]
Q8N128	Protein FAM177A1 OS=Homo sapiens GN=FAM177A1 PE=1 SV=1 - [F177A_HUMAN]
Q6ZUX3	Protein FAM179A OS=Homo sapiens GN=FAM179A PE=2 SV=2 - [F179A_HUMAN]
Q9Y4F4	Protein FAM179B OS=Homo sapiens GN=FAM179B PE=1 SV=4 - [F179B_HUMAN]
Q8IYM0	Protein FAM186B OS=Homo sapiens GN=FAM186B PE=2 SV=2 - [F186B_HUMAN]
Q96PV7	Protein FAM193B OS=Homo sapiens GN=FAM193B PE=1 SV=3 - [F193B_HUMAN]
Q96KR6	Protein FAM210B OS=Homo sapiens GN=FAM210B PE=1 SV=2 - [F210B_HUMAN]
Q32MH5	Protein FAM214A OS=Homo sapiens GN=FAM214A PE=1 SV=2 - [F214A_HUMAN]
Q7Z4H9	Protein FAM220A OS=Homo sapiens GN=FAM220A PE=2 SV=1 - [F220A_HUMAN]
Q8WU58	Protein FAM222B OS=Homo sapiens GN=FAM222B PE=2 SV=1 - [F222B_HUMAN]
Q5JW98	Protein FAM26D OS=Homo sapiens GN=FAM26D PE=2 SV=1 - [FA26D_HUMAN]
Q86V20	Protein FAM35A OS=Homo sapiens GN=FAM35A PE=2 SV=1 - [FA35A_HUMAN]
Q96BQ1	Protein FAM3D OS=Homo sapiens GN=FAM3D PE=1 SV=1 - [FAM3D_HUMAN]
Q96A09	Protein FAM46B OS=Homo sapiens GN=FAM46B PE=1 SV=2 - [FA46B_HUMAN]
Q6ZV65	Protein FAM47E OS=Homo sapiens GN=FAM47E PE=2 SV=3 - [FA47E_HUMAN]
Q8N5Q1	Protein FAM71E2 OS=Homo sapiens GN=FAM71E2 PE=2 SV=3 - [F71E2_HUMAN]
Q96LP2	Protein FAM81B OS=Homo sapiens GN=FAM81B PE=1 SV=3 - [FA81B_HUMAN]
Q96KN1	Protein FAM84B OS=Homo sapiens GN=FAM84B PE=1 SV=1 - [FA84B_HUMAN]
Q68CZ1	Protein fantom OS=Homo sapiens GN=RPGRIP1L PE=1 SV=2 - [FTM_HUMAN]
Q9UK73	Protein fem-1 homolog B OS=Homo sapiens GN=FEM1B PE=1 SV=1 - [FEM1B_HUMAN]
Q5TBA9	Protein furry homolog OS=Homo sapiens GN=FRY PE=1 SV=1 - [FRY_HUMAN]
O94915	Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2 - [FRYL_HUMAN]
Q96NT3	Protein GUCD1 OS=Homo sapiens GN=GUCD1 PE=1 SV=2 - [GUCD1_HUMAN]
Q9BTY7	Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1 - [HGH1_HUMAN]
Q9NQC1	Protein Jade-2 OS=Homo sapiens GN=JADE2 PE=1 SV=2 - [JADE2_HUMAN]
Q92613	Protein Jade-3 OS=Homo sapiens GN=JADE3 PE=1 SV=1 - [JADE3_HUMAN]
Q92833	Protein Jumonji OS=Homo sapiens GN=JARID2 PE=1 SV=2 - [JARD2_HUMAN]
Q04759	Protein kinase C theta type OS=Homo sapiens GN=PRKCQ PE=1 SV=3 - [KPCT_HUMAN]
Q7Z429	Protein lifeguard 1 OS=Homo sapiens GN=GRINA PE=2 SV=1 - [LFG1_HUMAN]
Q8N485	Protein limb expression 1 homolog OS=Homo sapiens GN=LIX1 PE=2 SV=2 - [LIX1_HUMAN]
Q9H9Z2	Protein lin-28 homolog A OS=Homo sapiens GN=LIN28A PE=1 SV=1 - [LN28A_HUMAN]

Q6UX01	Protein LMBR1L OS=Homo sapiens GN=LMBR1L PE=1 SV=2 - [LMBRL_HUMAN]
Q7Z4T9	Protein MAATS1 OS=Homo sapiens GN=MAATS1 PE=1 SV=2 - [MAAT1_HUMAN]
Q6ZRQ5	Protein MMS22-like OS=Homo sapiens GN=MMS22L PE=1 SV=3 - [MMS22_HUMAN]
Q9P2P1	Protein NYNRIN OS=Homo sapiens GN=NYNRIN PE=2 SV=3 - [NYNRI_HUMAN]
Q8NBL1	Protein O-glucosyltransferase 1 OS=Homo sapiens GN=POGLUT1 PE=1 SV=1 - [PGLT1_HUMAN]
Q13438	Protein OS-9 OS=Homo sapiens GN=OS9 PE=1 SV=1 - [OS9_HUMAN]
Q86TB9	Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 PE=1 SV=2 - [PATL1_HUMAN]
Q13635	Protein patched homolog 1 OS=Homo sapiens GN=PTCH1 PE=1 SV=2 - [PTC1_HUMAN]
O14974	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1 - [MYPT1_HUMAN]
Q9NXH3	Protein phosphatase 1 regulatory subunit 14D OS=Homo sapiens GN=PPP1R14D PE=1 SV=1 - [PP14D_HUMAN]
O75807	Protein phosphatase 1 regulatory subunit 15A OS=Homo sapiens GN=PPP1R15A PE=1 SV=1 - [PR15A_HUMAN]
Q5SWA1	Protein phosphatase 1 regulatory subunit 15B OS=Homo sapiens GN=PPP1R15B PE=1 SV=1 - [PR15B_HUMAN]
Q96LQ0	Protein phosphatase 1 regulatory subunit 36 OS=Homo sapiens GN=PPP1R36 PE=1 SV=1 - [PPR36_HUMAN]
Q9UQK1	Protein phosphatase 1 regulatory subunit 3C OS=Homo sapiens GN=PPP1R3C PE=1 SV=2 - [PPR3C_HUMAN]
Q5JR12	Protein phosphatase 1J OS=Homo sapiens GN=PPM1J PE=1 SV=1 - [PPM1J_HUMAN]
Q8WYL5	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens GN=SSH1 PE=1 SV=2 - [SSH1_HUMAN]
Q8TE77	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2 - [SSH3_HUMAN]
P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 - [S10A8_HUMAN]
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]
P25815	Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2 - [S100P_HUMAN]
Q99590	Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 - [SCAFB_HUMAN]
Q8N9R8	Protein SCAI OS=Homo sapiens GN=SCAI PE=1 SV=2 - [SCAI_HUMAN]
Q14160	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN]
Q9UBV2	Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3 - [SE1L1_HUMAN]
Q5TEA6	Protein sel-1 homolog 2 OS=Homo sapiens GN=SEL1L2 PE=1 SV=2 - [SE1L2_HUMAN]
Q96JX3	Protein SERAC1 OS=Homo sapiens GN=SERAC1 PE=1 SV=1 - [SRAC1_HUMAN]
Q8TF72	Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2 - [SHRM3_HUMAN]
Q7Z5N4	Protein sidekick-1 OS=Homo sapiens GN=SDK1 PE=2 SV=3 - [SDK1_HUMAN]
O94964	Protein SOGA1 OS=Homo sapiens GN=SOGA1 PE=1 SV=2 - [SOGA1_HUMAN]
Q5TF21	Protein SOGA3 OS=Homo sapiens GN=SOGA3 PE=3 SV=1 - [SOGA3_HUMAN]
O43597	Protein sprouty homolog 2 OS=Homo sapiens GN=SPRY2 PE=1 SV=1 - [SPY2_HUMAN]
A3KN83	Protein strawberry notch homolog 1 OS=Homo sapiens GN=SBNO1 PE=1 SV=1 - [SBNO1_HUMAN]
Q9HCD6	Protein TANC2 OS=Homo sapiens GN=TANC2 PE=1 SV=3 - [TANC2_HUMAN]
Q86X45	Protein tilB homolog OS=Homo sapiens GN=LRRC6 PE=1 SV=3 - [TILB_HUMAN]
Q9UNS1	Protein timeless homolog OS=Homo sapiens GN=TIMELESS PE=1 SV=2 - [TIM_HUMAN]
Q969W9	Protein TMEPAI OS=Homo sapiens GN=PMEPA1 PE=1 SV=1 - [PMEPA_HUMAN]
O95487	Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2 - [SC24B_HUMAN]
Q9UPX0	Protein turtle homolog B OS=Homo sapiens GN=IGSF9B PE=2 SV=2 - [TUTLB_HUMAN]
O14795	Protein unc-13 homolog B OS=Homo sapiens GN=UNC13B PE=1 SV=2 - [UN13B_HUMAN]
Q8NB66	Protein unc-13 homolog C OS=Homo sapiens GN=UNC13C PE=2 SV=3 - [UN13C_HUMAN]
Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN]
Q8IWX7	Protein unc-45 homolog B OS=Homo sapiens GN=UNC45B PE=1 SV=1 - [UN45B_HUMAN]
Q9P2D8	Protein unc-79 homolog OS=Homo sapiens GN=UNC79 PE=2 SV=4 - [UNC79_HUMAN]
Q8N2C7	Protein unc-80 homolog OS=Homo sapiens GN=UNC80 PE=2 SV=2 - [UNC80_HUMAN]
Q8NEX6	Protein WFDC11 OS=Homo sapiens GN=WFDC11 PE=3 SV=1 - [WFD11_HUMAN]
Q9ULE0	Protein WWC3 OS=Homo sapiens GN=WWC3 PE=1 SV=3 - [WWC3_HUMAN]
Q9GZM5	Protein YIPF3 OS=Homo sapiens GN=YIPF3 PE=1 SV=1 - [YIPF3_HUMAN]
P62699	Protein yippee-like 5 OS=Homo sapiens GN=YPEL5 PE=1 SV=1 - [YPEL5_HUMAN]

Q70YC5	Protein ZNF365 OS=Homo sapiens GN=ZNF365 PE=1 SV=3 - [ZN365_HUMAN]
Q8NE65	Protein ZNF738 OS=Homo sapiens GN=ZNF738 PE=2 SV=1 - [ZN738_HUMAN]
Q9C0D3	Protein zyg-11 homolog B OS=Homo sapiens GN=ZYG11B PE=1 SV=2 - [ZY11B_HUMAN]
Q96RI0	Proteinase-activated receptor 4 OS=Homo sapiens GN=F2RL3 PE=1 SV=3 - [PAR4_HUMAN]
Q9H867	Protein-lysine methyltransferase METTL21D OS=Homo sapiens GN=VCPKMT PE=1 SV=2 - [MT21D_HUMAN]
O60507	Protein-tyrosine sulfotransferase 1 OS=Homo sapiens GN=TPST1 PE=2 SV=1 - [TPST1_HUMAN]
Q92954	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2 - [PRG4_HUMAN]
P06454	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2 - [PTMA_HUMAN]
Q9Y5H7	Protocadherin alpha-5 OS=Homo sapiens GN=PCDHA5 PE=2 SV=1 - [PCDA5_HUMAN]
Q9NRJ7	Protocadherin beta-16 OS=Homo sapiens GN=PCDHB16 PE=1 SV=3 - [PCDBG_HUMAN]
Q6V0I7	Protocadherin Fat 4 OS=Homo sapiens GN=FAT4 PE=1 SV=2 - [FAT4_HUMAN]
Q9Y5H1	Protocadherin gamma-A2 OS=Homo sapiens GN=PCDHGA2 PE=2 SV=1 - [PCDG2_HUMAN]
Q9Y5F9	Protocadherin gamma-B6 OS=Homo sapiens GN=PCDHGB6 PE=2 SV=1 - [PCDGI_HUMAN]
Q96JQ0	Protocadherin-16 OS=Homo sapiens GN=DCHS1 PE=1 SV=1 - [PCD16_HUMAN]
Q8TAB3	Protocadherin-19 OS=Homo sapiens GN=PCDH19 PE=1 SV=3 - [PCD19_HUMAN]
Q8N6Y1	Protocadherin-20 OS=Homo sapiens GN=PCDH20 PE=2 SV=2 - [PCD20_HUMAN]
Q96QE2	Proton myo-inositol cotransporter OS=Homo sapiens GN=SLC2A13 PE=1 SV=3 - [MYCT_HUMAN]
P04201	Proto-oncogene Mas OS=Homo sapiens GN=MAS1 PE=1 SV=1 - [MAS_HUMAN]
P15498	Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=4 - [VAV_HUMAN]
P04628	Proto-oncogene Wnt-1 OS=Homo sapiens GN=WNT1 PE=1 SV=1 - [WNT1_HUMAN]
Q9H792	Pseudopodium-enriched atypical kinase 1 OS=Homo sapiens GN=PEAK1 PE=1 SV=4 - [PEAK1_HUMAN]
P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]
Q92771	Putative ATP-dependent RNA helicase DDX12 OS=Homo sapiens GN=DDX12P PE=5 SV=3 - [DDX12_HUMAN]
Q9BYX7	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]
Q9NP73	Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13 OS=Homo sapiens GN=ALG13 PE=1 SV=2 - [ALG13_HUMAN]
Q6NXN4	Putative C-mannosyltransferase DPY19L2P1 OS=Homo sapiens GN=DPY19L2P1 PE=2 SV=1 - [D19P1_HUMAN]
Q8IX95	Putative cTAGE family member 3 OS=Homo sapiens GN=CTAGE3P PE=5 SV=1 - [CTGE3_HUMAN]
A0A087X1C5	Putative cytochrome P450 2D7 OS=Homo sapiens GN=CYP2D7 PE=5 SV=1 - [CP2D7_HUMAN]
P0CG22	Putative dehydrogenase/reductase SDR family member 4-like 1 OS=Homo sapiens GN=DHRS4L1 PE=5 SV=1 - [DR4L1_HUMAN]
Q8N806	Putative E3 ubiquitin-protein ligase UBR7 OS=Homo sapiens GN=UBR7 PE=1 SV=2 - [UBR7_HUMAN]
Q5T036	Putative FAM120A opposite strand protein OS=Homo sapiens GN=FAM120AOS PE=5 SV=1 - [F120S_HUMAN]
Q9BXT6	Putative helicase Mov10l1 OS=Homo sapiens GN=MOV10L1 PE=2 SV=1 - [M10L1_HUMAN]
Q9NQX0	Putative histone-lysine N-methyltransferase PRDM6 OS=Homo sapiens GN=PRDM6 PE=2 SV=2 - [PRDM6_HUMAN]
Q8N3S3	Putative homeodomain transcription factor 2 OS=Homo sapiens GN=PHTF2 PE=2 SV=2 - [PHTF2_HUMAN]
A6NCN2	Putative keratin-87 protein OS=Homo sapiens GN=KRT87P PE=5 SV=4 - [KR87P_HUMAN]
Q5JSQ8	Putative KHDC1-like protein OS=Homo sapiens GN=KHDC1L PE=5 SV=1 - [KHDCL_HUMAN]
Q8NE18	Putative methyltransferase NSUN7 OS=Homo sapiens GN=NSUN7 PE=2 SV=4 - [NSUN7_HUMAN]
Q49A26	Putative oxidoreductase GLYR1 OS=Homo sapiens GN=GLYR1 PE=1 SV=3 - [GLYR1_HUMAN]
A2A3N6	Putative PIP5K1A and PSMD4-like protein OS=Homo sapiens GN=PIPSL PE=5 SV=1 - [PIPSL_HUMAN]
Q9C0F0	Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3 - [ASXL3_HUMAN]
A6NNC1	Putative POM121-like protein 1-like OS=Homo sapiens PE=5 SV=3 - [P12LL_HUMAN]
A4D2B8	Putative postmeiotic segregation increased 2-like protein 1 OS=Homo sapiens GN=PMS2P1 PE=5 SV=1 - [PM2P1_HUMAN]
P0DMR3	Putative protein ATXN8OS OS=Homo sapiens GN=ATXN8OS PE=5 SV=1 - [AT8OS_HUMAN]
O60756	Putative protein BCE-1 OS=Homo sapiens GN=BCE1 PE=5 SV=1 - [BCE1_HUMAN]
A6NHR8	Putative protein FAM47D OS=Homo sapiens GN=FAM47DP PE=5 SV=3 - [FA47D_HUMAN]
Q8IXW5	Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 OS=Homo sapiens GN=RPAP2 PE=1 SV=1 - [RPAP2_HUMAN]
Q8NDT2	Putative RNA-binding protein 15B OS=Homo sapiens GN=RBM15B PE=1 SV=3 - [RB15B_HUMAN]
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2 - [LC7L2_HUMAN]
Q9GZW5	Putative SCAN domain-containing protein SCAND2P OS=Homo sapiens GN=SCAND2P PE=5 SV=2 -

	[SCND2_HUMAN]
Q08AI6	Putative sodium-coupled neutral amino acid transporter 11 OS=Homo sapiens GN=SLC38A11 PE=2 SV=1 - [S38AB_HUMAN]
A6NKX4	Putative solute carrier family 22 member 31 OS=Homo sapiens GN=SLC22A31 PE=3 SV=3 - [S22AV_HUMAN]
P0C874	Putative spermatogenesis-associated protein 31D3 OS=Homo sapiens GN=SPATA31D3 PE=5 SV=1 - [S31D3_HUMAN]
Q9H489	Putative testis-specific Y-encoded-like protein 3 OS=Homo sapiens GN=TSPY26P PE=5 SV=1 - [TSY26_HUMAN]
Q8IY50	Putative thiamine transporter SLC35F3 OS=Homo sapiens GN=SLC35F3 PE=2 SV=2 - [S35F3_HUMAN]
O14753	Putative transcription factor Ovo-like 1 OS=Homo sapiens GN=OVOL1 PE=2 SV=3 - [OVOL1_HUMAN]
P0C7V6	Putative transcription factor SPT20 homolog-like 2 OS=Homo sapiens GN=SUPT20HL2 PE=5 SV=1 - [SP202_HUMAN]
A8K010	Putative transcriptional regulator encoded by LINC00473 OS=Homo sapiens GN=LINC00473 PE=5 SV=2 - [CF176_HUMAN]
A6NLI5	Putative tripartite motif-containing protein 64C OS=Homo sapiens GN=TRIM64C PE=5 SV=3 - [TR64C_HUMAN]
Q495Z4	Putative uncharacterized protein ASB16-AS1 OS=Homo sapiens GN=ASB16-AS1 PE=5 SV=2 - [ASAS1_HUMAN]
Q8TAV5	Putative uncharacterized protein C11orf45 OS=Homo sapiens GN=C11orf45 PE=2 SV=1 - [CK045_HUMAN]
Q6ZS72	Putative uncharacterized protein C19orf35 OS=Homo sapiens GN=C19orf35 PE=2 SV=1 - [CS035_HUMAN]
Q9NVV2	Putative uncharacterized protein C19orf73 OS=Homo sapiens GN=C19orf73 PE=1 SV=2 - [CS073_HUMAN]
B1AJZ1	Putative uncharacterized protein C1orf196 OS=Homo sapiens GN=C1orf196 PE=5 SV=2 - [CA196_HUMAN]
Q6ZS94	Putative uncharacterized protein C1orf229 OS=Homo sapiens GN=C1orf229 PE=2 SV=1 - [CA229_HUMAN]
A6NFR6	Putative uncharacterized protein C5orf60 OS=Homo sapiens GN=C5orf60 PE=1 SV=2 - [CE060_HUMAN]
A4D174	Putative uncharacterized protein C7orf71 OS=Homo sapiens GN=C7orf71 PE=2 SV=1 - [CG071_HUMAN]
Q96LI9	Putative uncharacterized protein CXorf58 OS=Homo sapiens GN=CXorf58 PE=2 SV=2 - [CX058_HUMAN]
A6NH13	Putative uncharacterized protein DNAJC9-AS1 OS=Homo sapiens GN=DNAJC9-AS1 PE=2 SV=2 - [DAS1_HUMAN]
Q6ZNR8	Putative uncharacterized protein encoded by LINC00176 OS=Homo sapiens GN=LINC00176 PE=5 SV=1 - [PRR17_HUMAN]
Q5T6M2	Putative uncharacterized protein encoded by LINC00242 OS=Homo sapiens GN=LINC00242 PE=5 SV=1 - [CF122_HUMAN]
Q6ZUF6	Putative uncharacterized protein encoded by LINC00336 OS=Homo sapiens GN=LINC00336 PE=5 SV=1 - [NC336_HUMAN]
Q8NI28	Putative uncharacterized protein encoded by LINC01006 OS=Homo sapiens GN=LINC01006 PE=5 SV=1 - [CG013_HUMAN]
Q9H7H1	Putative uncharacterized protein encoded by RUNX1-IT1 OS=Homo sapiens GN=RUNX1-IT1 PE=2 SV=1 - [RUIT1_HUMAN]
A8MVM7	Putative uncharacterized protein ENSP00000382790 OS=Homo sapiens PE=5 SV=3 - [YD021_HUMAN]
Q8NA97	Putative uncharacterized protein FER1L6-AS1 OS=Homo sapiens GN=FER1L6-AS1 PE=2 SV=1 - [FEAS1_HUMAN]
Q8N1Y9	Putative uncharacterized protein FLJ37218 OS=Homo sapiens PE=5 SV=2 - [YI025_HUMAN]
Q6ZSR6	Putative uncharacterized protein FLJ45256 OS=Homo sapiens PE=2 SV=3 - [YP007_HUMAN]
Q8IYB0	Putative uncharacterized protein MGC39545 OS=Homo sapiens PE=5 SV=2 - [YK038_HUMAN]
Q0IIN9	Putative uncharacterized protein ZNF252P-AS1 OS=Homo sapiens GN=ZNF252P-AS1 PE=5 SV=1 - [ZNFS1_HUMAN]
A6NL46	Putative UPF0607 protein ENSP00000332738 OS=Homo sapiens PE=3 SV=3 - [YF016_HUMAN]
A8MU76	Putative UPF0607 protein ENSP00000381418 OS=Homo sapiens PE=3 SV=2 - [YP034_HUMAN]
Q8N9G6	Putative UPF0607 protein FLJ37424 OS=Homo sapiens PE=2 SV=1 - [YJ012_HUMAN]
Q92670	Putative zinc finger protein 75C OS=Homo sapiens GN=ZNF75CP PE=5 SV=2 - [ZN75C_HUMAN]
Q6ZT77	Putative zinc finger protein 826 OS=Homo sapiens GN=ZNF826P PE=5 SV=2 - [ZN826_HUMAN]
Q8WU10	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=PYROXD1 PE=1 SV=1 - [PYRD1_HUMAN]
Q8TCD6	Pyridoxal phosphate phosphatase PHOSPHO2 OS=Homo sapiens GN=PHOSPHO2 PE=1 SV=1 - [PHOP2_HUMAN]
A6NFU8	Pyroglutamyl-peptidase 1-like protein OS=Homo sapiens GN=PGPEP1L PE=2 SV=4 - [PGPIL_HUMAN]
P30613	Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]
Q9H974	Queuine tRNA-ribosyltransferase subunit QTRTD1 OS=Homo sapiens GN=QTRTD1 PE=1 SV=1 - [QTRD1_HUMAN]
Q9Y2K5	R3H domain-containing protein 2 OS=Homo sapiens GN=R3HDM2 PE=1 SV=3 - [R3HD2_HUMAN]
Q8NFW9	Rab effector MyRIP OS=Homo sapiens GN=MYRIP PE=1 SV=2 - [MYRIP_HUMAN]
Q5HYI8	Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1 - [RABL3_HUMAN]

Q86UC2	Radial spoke head protein 3 homolog OS=Homo sapiens GN=RSPH3 PE=1 SV=1 - [RSPH3_HUMAN]
P46695	Radiation-inducible immediate-early gene IEX-1 OS=Homo sapiens GN=IER3 PE=1 SV=4 - [IEX1_HUMAN]
Q14699	Raftlin OS=Homo sapiens GN=RFTN1 PE=1 SV=4 - [RFTN1_HUMAN]
Q86X10	Ral GTPase-activating protein subunit beta OS=Homo sapiens GN=RALGAPB PE=1 SV=1 - [RLGPB_HUMAN]
Q9NZL6	Ral guanine nucleotide dissociation stimulator-like 1 OS=Homo sapiens GN=RGL1 PE=1 SV=1 - [RGL1_HUMAN]
Q96D71	RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1 PE=1 SV=3 - [REPS1_HUMAN]
Q8NFH8	RalBP1-associated Eps domain-containing protein 2 OS=Homo sapiens GN=REPS2 PE=1 SV=2 - [REPS2_HUMAN]
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]
Q6VN20	Ran-binding protein 10 OS=Homo sapiens GN=RANBP10 PE=1 SV=1 - [RBP10_HUMAN]
Q9H2T7	Ran-binding protein 17 OS=Homo sapiens GN=RANBP17 PE=2 SV=1 - [RBP17_HUMAN]
O60518	Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2 - [RNBP6_HUMAN]
P0DJD0	RANBP2-like and GRIP domain-containing protein 1 OS=Homo sapiens GN=RGPD1 PE=2 SV=1 - [RGPD1_HUMAN]
Q7Z3J3	RanBP2-like and GRIP domain-containing protein 4 OS=Homo sapiens GN=RGPD4 PE=2 SV=3 - [RGPD4_HUMAN]
Q9UHV5	Rap guanine nucleotide exchange factor-like 1 OS=Homo sapiens GN=RAPGEFL1 PE=1 SV=2 - [RPGFL_HUMAN]
Q684P5	Rap1 GTPase-activating protein 2 OS=Homo sapiens GN=RAP1GAP2 PE=1 SV=2 - [RPGP2_HUMAN]
Q8WWW0	Ras association domain-containing protein 5 OS=Homo sapiens GN=RASSF5 PE=1 SV=1 - [RASF5_HUMAN]
Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]
Q86VI3	Ras GTPase-activating-like protein IQGAP3 OS=Homo sapiens GN=IQGAP3 PE=1 SV=2 - [IQGA3_HUMAN]
O95267	RAS guanyl-releasing protein 1 OS=Homo sapiens GN=RASGRP1 PE=1 SV=2 - [GRP1_HUMAN]
P60763	Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens GN=RAC3 PE=1 SV=1 - [RAC3_HUMAN]
Q9NX57	Ras-related protein Rab-20 OS=Homo sapiens GN=RAB20 PE=1 SV=1 - [RAB20_HUMAN]
Q9ULW5	Ras-related protein Rab-26 OS=Homo sapiens GN=RAB26 PE=1 SV=3 - [RAB26_HUMAN]
Q14088	Ras-related protein Rab-33A OS=Homo sapiens GN=RAB33A PE=1 SV=2 - [RB33A_HUMAN]
P20337	Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2 - [RAB3B_HUMAN]
Q8TDY2	RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3 - [RBCC1_HUMAN]
Q13127	RE1-silencing transcription factor OS=Homo sapiens GN=REST PE=1 SV=3 - [REST_HUMAN]
P04626	Receptor tyrosine-protein kinase erbB-2 OS=Homo sapiens GN=ERBB2 PE=1 SV=1 - [ERBB2_HUMAN]
P57078	Receptor-interacting serine/threonine-protein kinase 4 OS=Homo sapiens GN=RIPK4 PE=1 SV=1 - [RIPK4_HUMAN]
P36888	Receptor-type tyrosine-protein kinase FLT3 OS=Homo sapiens GN=FLT3 PE=1 SV=2 - [FLT3_HUMAN]
P18433	Receptor-type tyrosine-protein phosphatase alpha OS=Homo sapiens GN=PTPRA PE=1 SV=2 - [PTPRA_HUMAN]
P23467	Receptor-type tyrosine-protein phosphatase beta OS=Homo sapiens GN=PTPRB PE=1 SV=3 - [PTPRB_HUMAN]
P23468	Receptor-type tyrosine-protein phosphatase delta OS=Homo sapiens GN=PTPRD PE=1 SV=2 - [PTPRD_HUMAN]
P28827	Receptor-type tyrosine-protein phosphatase mu OS=Homo sapiens GN=PTPRM PE=1 SV=2 - [PTPRM_HUMAN]
Q92932	Receptor-type tyrosine-protein phosphatase N2 OS=Homo sapiens GN=PTPRN2 PE=1 SV=2 - [PTPR2_HUMAN]
P23471	Receptor-type tyrosine-protein phosphatase zeta OS=Homo sapiens GN=PTPRZ1 PE=1 SV=4 - [PTPRZ_HUMAN]
P35243	Recoverin OS=Homo sapiens GN=RCVRN PE=1 SV=2 - [RECO_HUMAN]
Q96E14	RecQ-mediated genome instability protein 2 OS=Homo sapiens GN=RMI2 PE=1 SV=2 - [RMI2_HUMAN]
Q86UR5	Regulating synaptic membrane exocytosis protein 1 OS=Homo sapiens GN=RIMS1 PE=1 SV=1 - [RIMS1_HUMAN]
Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A OS=Homo sapiens GN=RPRD1A PE=1 SV=1 - [RPR1A_HUMAN]
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2 OS=Homo sapiens GN=RPRD2 PE=1 SV=1 - [RPRD2_HUMAN]
O94810	Regulator of G-protein signaling 11 OS=Homo sapiens GN=RGS11 PE=1 SV=2 - [RGS11_HUMAN]
O14924	Regulator of G-protein signaling 12 OS=Homo sapiens GN=RGS12 PE=1 SV=1 - [RGS12_HUMAN]
Q8NE09	Regulator of G-protein signaling 22 OS=Homo sapiens GN=RGS22 PE=1 SV=3 - [RGS22_HUMAN]
P49758	Regulator of G-protein signaling 6 OS=Homo sapiens GN=RGS6 PE=1 SV=5 - [RGS6_HUMAN]

Q92900	Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2 - [RENT1_HUMAN]
P00797	Renin OS=Homo sapiens GN=REN PE=1 SV=1 - [RENI_HUMAN]
O75787	Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=1 SV=2 - [RENR_HUMAN]
P40938	Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2 - [RFC3_HUMAN]
P40937	Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=1 SV=1 - [RFC5_HUMAN]
Q9NWS8	Required for meiotic nuclear division protein 1 homolog OS=Homo sapiens GN=RMND1 PE=1 SV=2 - [RMND1_HUMAN]
Q16799	Reticulon-1 OS=Homo sapiens GN=RTN1 PE=1 SV=1 - [RTN1_HUMAN]
P78363	Retinal-specific ATP-binding cassette transporter OS=Homo sapiens GN=ABCA4 PE=1 SV=3 - [ABCA4_HUMAN]
P06400	Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 - [RB_HUMAN]
P28749	Retinoblastoma-like protein 1 OS=Homo sapiens GN=RBL1 PE=1 SV=3 - [RBL1_HUMAN]
P10276	Retinoic acid receptor alpha OS=Homo sapiens GN=RARA PE=1 SV=2 - [RARA_HUMAN]
P10826	Retinoic acid receptor beta OS=Homo sapiens GN=RARB PE=1 SV=2 - [RARB_HUMAN]
Q9UL19	Retinoic acid receptor responder protein 3 OS=Homo sapiens GN=RARRES3 PE=1 SV=1 - [HRSL4_HUMAN]
Q7Z5J4	Retinoic acid-induced protein 1 OS=Homo sapiens GN=RAI1 PE=1 SV=2 - [RAI1_HUMAN]
P10745	Retinol-binding protein 3 OS=Homo sapiens GN=RBP3 PE=1 SV=2 - [RET3_HUMAN]
Q5T5U3	Rho GTPase-activating protein 21 OS=Homo sapiens GN=ARHGAP21 PE=1 SV=1 - [RHG21_HUMAN]
Q9P227	Rho GTPase-activating protein 23 OS=Homo sapiens GN=ARHGAP23 PE=1 SV=2 - [RHG23_HUMAN]
Q52LW3	Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=1 SV=2 - [RHG29_HUMAN]
Q9NRY4	Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3 - [RHG35_HUMAN]
Q6ZRI8	Rho GTPase-activating protein 36 OS=Homo sapiens GN=ARHGAP36 PE=2 SV=1 - [RHG36_HUMAN]
Q9C0H5	Rho GTPase-activating protein 39 OS=Homo sapiens GN=ARHGAP39 PE=1 SV=2 - [RHG39_HUMAN]
Q9BRR9	Rho GTPase-activating protein 9 OS=Homo sapiens GN=ARHGAP9 PE=1 SV=2 - [RHG09_HUMAN]
Q92888	Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=1 SV=2 - [ARHG1_HUMAN]
Q96PE2	Rho guanine nucleotide exchange factor 17 OS=Homo sapiens GN=ARHGEF17 PE=1 SV=1 - [ARHGH_HUMAN]
Q8IW93	Rho guanine nucleotide exchange factor 19 OS=Homo sapiens GN=ARHGEF19 PE=1 SV=1 - [ARHGJ_HUMAN]
A5YM69	Rho guanine nucleotide exchange factor 35 OS=Homo sapiens GN=ARHGEF35 PE=1 SV=1 - [ARG35_HUMAN]
Q12774	Rho guanine nucleotide exchange factor 5 OS=Homo sapiens GN=ARHGEF5 PE=1 SV=3 - [ARHG5_HUMAN]
P61587	Rho-related GTP-binding protein RhoE OS=Homo sapiens GN=RND3 PE=1 SV=1 - [RND3_HUMAN]
Q8IY67	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 - [RAVR1_HUMAN]
O75582	Ribosomal protein S6 kinase alpha-5 OS=Homo sapiens GN=RPS6KA5 PE=1 SV=1 - [KS6A5_HUMAN]
Q9UK32	Ribosomal protein S6 kinase alpha-6 OS=Homo sapiens GN=RPS6KA6 PE=1 SV=1 - [KS6A6_HUMAN]
Q9H7B2	Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1 SV=2 - [RPF2_HUMAN]
O94941	RING finger protein 37 OS=Homo sapiens GN=UBOX5 PE=1 SV=1 - [RNF37_HUMAN]
Q96E39	RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1 - [RMXL1_HUMAN]
Q9GZR2	RNA exonuclease 4 OS=Homo sapiens GN=REXO4 PE=1 SV=2 - [REXO4_HUMAN]
P55199	RNA polymerase II elongation factor ELL OS=Homo sapiens GN=ELL PE=1 SV=1 - [ELL_HUMAN]
Q92541	RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens GN=RTF1 PE=1 SV=4 - [RTF1_HUMAN]
Q5U5Q3	RNA-binding E3 ubiquitin-protein ligase MEX3C OS=Homo sapiens GN=MEX3C PE=1 SV=3 - [MEX3C_HUMAN]
O75526	RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens GN=RBMXL2 PE=1 SV=3 - [RMXL2_HUMAN]
Q8N7X1	RNA-binding motif protein, X-linked-like-3 OS=Homo sapiens GN=RBMXL3 PE=2 SV=2 - [RMXL3_HUMAN]
A6NDE4	RNA-binding motif protein, Y chromosome, family 1 member B OS=Homo sapiens GN=RBMY1B PE=2 SV=2 - [RBY1B_HUMAN]
P29558	RNA-binding motif, single-stranded-interacting protein 1 OS=Homo sapiens GN=RBMS1 PE=1 SV=3 - [RBMS1_HUMAN]
Q15434	RNA-binding motif, single-stranded-interacting protein 2 OS=Homo sapiens GN=RBMS2 PE=1 SV=1 - [RBMS2_HUMAN]
P98175	RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3 - [RBM10_HUMAN]
Q5T481	RNA-binding protein 20 OS=Homo sapiens GN=RBM20 PE=1 SV=3 - [RBM20_HUMAN]
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 - [RBM25_HUMAN]
Q5T8P6	RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3 - [RBM26_HUMAN]

Q96EV2	RNA-binding protein 33 OS=Homo sapiens GN=RBM33 PE=1 SV=3 - [RBM33_HUMAN]
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]
Q01844	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [EWS_HUMAN]
Q15287	RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1 - [RNPS1_HUMAN]
Q5TZA2	Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1 - [CROCC_HUMAN]
Q5TC82	Roquin-1 OS=Homo sapiens GN=RC3H1 PE=1 SV=1 - [RC3H1_HUMAN]
Q96MS0	Roundabout homolog 3 OS=Homo sapiens GN=ROBO3 PE=1 SV=2 - [ROBO3_HUMAN]
Q6IN84	rRNA methyltransferase 1, mitochondrial OS=Homo sapiens GN=MRM1 PE=1 SV=1 - [MRM1_HUMAN]
Q9BVN2	RUN and SH3 domain-containing protein 1 OS=Homo sapiens GN=RUSC1 PE=1 SV=3 - [RUSC1_HUMAN]
Q96NL0	RUN domain-containing protein 3B OS=Homo sapiens GN=RUNDC3B PE=2 SV=1 - [RUN3B_HUMAN]
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]
P21817	Ryanodine receptor 1 OS=Homo sapiens GN=RYR1 PE=1 SV=3 - [RYR1_HUMAN]
Q92736	Ryanodine receptor 2 OS=Homo sapiens GN=RYR2 PE=1 SV=3 - [RYR2_HUMAN]
Q15413	Ryanodine receptor 3 OS=Homo sapiens GN=RYR3 PE=1 SV=3 - [RYR3_HUMAN]
Q8N5C6	S1 RNA-binding domain-containing protein 1 OS=Homo sapiens GN=SRBD1 PE=1 SV=2 - [SRBD1_HUMAN]
A6NKF1	SAC3 domain-containing protein 1 OS=Homo sapiens GN=SAC3D1 PE=1 SV=2 - [SAC31_HUMAN]
Q9NZJ4	Sacsin OS=Homo sapiens GN=SACS PE=1 SV=2 - [SACS_HUMAN]
P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 - [METK2_HUMAN]
Q9NWH9	SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2 - [SLTM_HUMAN]
O94885	SAM and SH3 domain-containing protein 1 OS=Homo sapiens GN=SASH1 PE=1 SV=3 - [SASH1_HUMAN]
Q14BN4	Sarcolemmal membrane-associated protein OS=Homo sapiens GN=SLMAP PE=1 SV=1 - [SLMAP_HUMAN]
Q9NXZ1	Sarcoma antigen 1 OS=Homo sapiens GN=SAGE1 PE=1 SV=2 - [SAGE1_HUMAN]
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN]
Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]
Q6R2W3	SCAN domain-containing protein 3 OS=Homo sapiens GN=ZBED9 PE=2 SV=1 - [SCND3_HUMAN]
Q6AZY7	Scavenger receptor class A member 3 OS=Homo sapiens GN=SCARA3 PE=1 SV=1 - [SCAR3_HUMAN]
Q7Z7L1	Schlafen family member 11 OS=Homo sapiens GN=SLFN11 PE=1 SV=2 - [SLN11_HUMAN]
P0C7P3	Schlafen family member 14 OS=Homo sapiens GN=SLFN14 PE=2 SV=2 - [SLN14_HUMAN]
Q08AF3	Schlafen family member 5 OS=Homo sapiens GN=SLFN5 PE=1 SV=1 - [SLFN5_HUMAN]
A2VEC9	SCO-spondin OS=Homo sapiens GN=SSPO PE=2 SV=1 - [SSPO_HUMAN]
O75711	Scrapie-responsive protein 1 OS=Homo sapiens GN=SCRG1 PE=1 SV=1 - [SCRG1_HUMAN]
Q6P3W7	SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1 - [SCYL2_HUMAN]
Q8WVM8	Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4 - [SCFD1_HUMAN]
Q8WU76	Sec1 family domain-containing protein 2 OS=Homo sapiens GN=SCFD2 PE=1 SV=2 - [SCFD2_HUMAN]
O76054	SEC14-like protein 2 OS=Homo sapiens GN=SEC14L2 PE=1 SV=1 - [S14L2_HUMAN]
Q9UDX4	SEC14-like protein 3 OS=Homo sapiens GN=SEC14L3 PE=1 SV=1 - [S14L3_HUMAN]
O43304	SEC14-like protein 5 OS=Homo sapiens GN=SEC14L5 PE=2 SV=3 - [S14L5_HUMAN]
Q9Y6Y8	SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1 - [S23IP_HUMAN]
Q8N474	Secreted frizzled-related protein 1 OS=Homo sapiens GN=SFRP1 PE=1 SV=1 - [SFRP1_HUMAN]
Q9BYH1	Seizure 6-like protein OS=Homo sapiens GN=SEZ6L PE=1 SV=1 - [SE6L1_HUMAN]
Q99985	Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=2 - [SEM3C_HUMAN]
O95025	Semaphorin-3D OS=Homo sapiens GN=SEMA3D PE=2 SV=2 - [SEM3D_HUMAN]
P04279	Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2 - [SEMG1_HUMAN]
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1 - [SEMG2_HUMAN]
Q9P0U3	Sentrin-specific protease 1 OS=Homo sapiens GN=SENP1 PE=1 SV=2 - [SENP1_HUMAN]
Q96HI0	Sentrin-specific protease 5 OS=Homo sapiens GN=SENP5 PE=1 SV=3 - [SENP5_HUMAN]
Q8WYJ6	Septin-1 OS=Homo sapiens GN=SEPT1 PE=1 SV=2 - [SEPT1_HUMAN]
Q9P0V9	Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2 - [SEP10_HUMAN]
Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]
Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]
O15270	Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1 - [SPTC2_HUMAN]

Q7RTY3	Serine protease 45 OS=Homo sapiens GN=PRSS45 PE=2 SV=1 - [PRS45_HUMAN]
Q8IYB3	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2 - [SRRM1_HUMAN]
Q9UQ35	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 - [SRRM2_HUMAN]
B3KS81	Serine/arginine repetitive matrix protein 5 OS=Homo sapiens GN=SRRM5 PE=1 SV=3 - [SRRM5_HUMAN]
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]
Q8WUJ0	Serine/threonine/tyrosine-interacting protein OS=Homo sapiens GN=STYX PE=1 SV=1 - [STYX_HUMAN]
P49842	Serine/threonine-protein kinase 19 OS=Homo sapiens GN=STK19 PE=1 SV=2 - [STK19_HUMAN]
Q9P289	Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2 - [STK26_HUMAN]
Q9BXU1	Serine/threonine-protein kinase 31 OS=Homo sapiens GN=STK31 PE=2 SV=2 - [STK31_HUMAN]
Q8WU08	Serine/threonine-protein kinase 32A OS=Homo sapiens GN=STK32A PE=1 SV=2 - [ST32A_HUMAN]
Q9BYT3	Serine/threonine-protein kinase 33 OS=Homo sapiens GN=STK33 PE=1 SV=1 - [STK33_HUMAN]
Q9NRP7	Serine/threonine-protein kinase 36 OS=Homo sapiens GN=STK36 PE=1 SV=2 - [STK36_HUMAN]
Q9BZL6	Serine/threonine-protein kinase D2 OS=Homo sapiens GN=PRKD2 PE=1 SV=2 - [KPCD2_HUMAN]
O94806	Serine/threonine-protein kinase D3 OS=Homo sapiens GN=PRKD3 PE=1 SV=1 - [KPCD3_HUMAN]
Q96Q04	Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=2 - [LMTK3_HUMAN]
P20794	Serine/threonine-protein kinase MAK OS=Homo sapiens GN=MAK PE=1 SV=2 - [MAK_HUMAN]
Q6DT37	Serine/threonine-protein kinase MRCK gamma OS=Homo sapiens GN=CDC42BPG PE=1 SV=2 - [MRCKG_HUMAN]
Q16513	Serine/threonine-protein kinase N2 OS=Homo sapiens GN=PKN2 PE=1 SV=1 - [PKN2_HUMAN]
P51957	Serine/threonine-protein kinase Nek4 OS=Homo sapiens GN=NEK4 PE=1 SV=2 - [NEK4_HUMAN]
Q8TDX7	Serine/threonine-protein kinase Nek7 OS=Homo sapiens GN=NEK7 PE=1 SV=1 - [NEK7_HUMAN]
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1 - [OXSR1_HUMAN]
Q13153	Serine/threonine-protein kinase PAK 1 OS=Homo sapiens GN=PAK1 PE=1 SV=2 - [PAK1_HUMAN]
O96013	Serine/threonine-protein kinase PAK 4 OS=Homo sapiens GN=PAK4 PE=1 SV=1 - [PAK4_HUMAN]
Q9BVS4	Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 PE=1 SV=2 - [RIOK2_HUMAN]
Q52WX2	Serine/threonine-protein kinase SBK1 OS=Homo sapiens GN=SBK1 PE=2 SV=1 - [SBK1_HUMAN]
Q96Q15	Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=1 SV=3 - [SMG1_HUMAN]
Q9H2K8	Serine/threonine-protein kinase TAO3 OS=Homo sapiens GN=TAOK3 PE=1 SV=2 - [TAOK3_HUMAN]
O75385	Serine/threonine-protein kinase ULK1 OS=Homo sapiens GN=ULK1 PE=1 SV=2 - [ULK1_HUMAN]
Q6PHR2	Serine/threonine-protein kinase ULK3 OS=Homo sapiens GN=ULK3 PE=1 SV=2 - [ULK3_HUMAN]
Q9Y3S1	Serine/threonine-protein kinase WNK2 OS=Homo sapiens GN=WNK2 PE=1 SV=4 - [WNK2_HUMAN]
Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform OS=Homo sapiens GN=PPP2R5E PE=1 SV=1 - [2A5E_HUMAN]
Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Homo sapiens GN=PPP2R5C PE=1 SV=3 - [2A5G_HUMAN]
P48454	Serine/threonine-protein phosphatase 2B catalytic subunit gamma isoform OS=Homo sapiens GN=PPP3CC PE=1 SV=3 - [PP2BC_HUMAN]
Q6NUP7	Serine/threonine-protein phosphatase 4 regulatory subunit 4 OS=Homo sapiens GN=PPP4R4 PE=1 SV=1 - [PP4R4_HUMAN]
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1 - [PPP6_HUMAN]
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5 - [PP6R1_HUMAN]
Q13315	Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=4 - [ATM_HUMAN]
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 - [TRFE_HUMAN]
P29508	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2 - [SPB3_HUMAN]
P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]
Q9NUC0	SERTA domain-containing protein 4 OS=Homo sapiens GN=SERTAD4 PE=2 SV=1 - [SRTD4_HUMAN]
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]
Q15166	Serum paraoxonase/lactonase 3 OS=Homo sapiens GN=PON3 PE=1 SV=3 - [PON3_HUMAN]
Q9Y6P5	Sestrin-1 OS=Homo sapiens GN=SESN1 PE=1 SV=2 - [SESN1_HUMAN]
Q9NVD3	SET domain-containing protein 4 OS=Homo sapiens GN=SETD4 PE=2 SV=1 - [SETD4_HUMAN]
Q9UBL3	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens GN=ASH2L PE=1 SV=1 - [ASH2L_HUMAN]
Q9UQR0	Sex comb on midleg-like protein 2 OS=Homo sapiens GN=SCML2 PE=1 SV=1 - [SCML2_HUMAN]
Q8N228	Sex comb on midleg-like protein 4 OS=Homo sapiens GN=SCML4 PE=1 SV=2 - [SCML4_HUMAN]
Q5VZ18	SH2 domain-containing adapter protein E OS=Homo sapiens GN=SHE PE=1 SV=1 - [SHE_HUMAN]

Q9H788	SH2 domain-containing protein 4A OS=Homo sapiens GN=SH2D4A PE=1 SV=1 - [SH24A_HUMAN]
Q9UPX8	SH3 and multiple ankyrin repeat domains protein 2 OS=Homo sapiens GN=SHANK2 PE=1 SV=3 - [SHAN2_HUMAN]
Q9BYB0	SH3 and multiple ankyrin repeat domains protein 3 OS=Homo sapiens GN=SHANK3 PE=1 SV=3 - [SHAN3_HUMAN]
Q5TCZ1	SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1 - [SPD2A_HUMAN]
Q9Y3L3	SH3 domain-binding protein 1 OS=Homo sapiens GN=SH3BP1 PE=1 SV=3 - [3BP1_HUMAN]
Q7L8J4	SH3 domain-binding protein 5-like OS=Homo sapiens GN=SH3BP5L PE=1 SV=1 - [3BP5L_HUMAN]
A4FU49	SH3 domain-containing protein 21 OS=Homo sapiens GN=SH3D21 PE=2 SV=2 - [SH321_HUMAN]
Q8NEM2	SHC SH2 domain-binding protein 1 OS=Homo sapiens GN=SHCBP1 PE=1 SV=3 - [SHCBP_HUMAN]
Q9UIL1	Short coiled-coil protein OS=Homo sapiens GN=SCOC PE=1 SV=2 - [SCOC_HUMAN]
A6NMB1	Sialic acid-binding Ig-like lectin 16 OS=Homo sapiens GN=SIGLEC16 PE=2 SV=3 - [SIG16_HUMAN]
Q9NYZ4	Sialic acid-binding Ig-like lectin 8 OS=Homo sapiens GN=SIGLEC8 PE=1 SV=2 - [SIGL8_HUMAN]
Q8WWR8	Sialidase-4 OS=Homo sapiens GN=NEU4 PE=1 SV=3 - [NEUR4_HUMAN]
Q5T5P2	Sickle tail protein homolog OS=Homo sapiens GN=KIAA1217 PE=1 SV=2 - [SKT_HUMAN]
Q96NB2	Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2 - [SFXN2_HUMAN]
Q9BWM7	Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2 - [SFXN3_HUMAN]
Q8TCT7	Signal peptide peptidase-like 2B OS=Homo sapiens GN=SPPL2B PE=1 SV=2 - [SPP2B_HUMAN]
Q9Y5M8	Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3 - [SRPRB_HUMAN]
P40763	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 - [STAT3_HUMAN]
O43166	Signal-induced proliferation-associated 1-like protein 1 OS=Homo sapiens GN=SIPA1L1 PE=1 SV=4 - [SI1L1_HUMAN]
Q9P2F8	Signal-induced proliferation-associated 1-like protein 2 OS=Homo sapiens GN=SIPA1L2 PE=1 SV=2 - [SI1L2_HUMAN]
Q5JXA9	Signal-regulatory protein beta-2 OS=Homo sapiens GN=SIRPB2 PE=2 SV=1 - [SIRB2_HUMAN]
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1 - [PDS5B_HUMAN]
Q9P0V8	SLAM family member 8 OS=Homo sapiens GN=SLAMF8 PE=1 SV=1 - [SLAF8_HUMAN]
Q96PX8	SLIT and NTRK-like protein 1 OS=Homo sapiens GN=SLITRK1 PE=1 SV=2 - [SLIK1_HUMAN]
Q9H5Y7	SLIT and NTRK-like protein 6 OS=Homo sapiens GN=SLITRK6 PE=2 SV=3 - [SLIK6_HUMAN]
O75093	Slit homolog 1 protein OS=Homo sapiens GN=SLIT1 PE=2 SV=4 - [SLIT1_HUMAN]
O75094	Slit homolog 3 protein OS=Homo sapiens GN=SLIT3 PE=2 SV=3 - [SLIT3_HUMAN]
O75044	SLIT-ROBO Rho GTPase-activating protein 2 OS=Homo sapiens GN=SRGAP2 PE=1 SV=2 - [SRGP2_HUMAN]
Q8TAD8	Smad nuclear-interacting protein 1 OS=Homo sapiens GN=SNIP1 PE=1 SV=1 - [SNIP1_HUMAN]
Q9H2S1	Small conductance calcium-activated potassium channel protein 2 OS=Homo sapiens GN=KCNN2 PE=1 SV=2 - [KCNN2_HUMAN]
P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1 - [RUXF_HUMAN]
P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]
Q5T8I9	Small RNA 2'-O-methyltransferase OS=Homo sapiens GN=HENMT1 PE=1 SV=1 - [HENMT_HUMAN]
Q8NHG7	Small VCP/p97-interacting protein OS=Homo sapiens GN=SVIP PE=1 SV=1 - [SVIP_HUMAN]
Q9Y4D2	Sn1-specific diacylglycerol lipase alpha OS=Homo sapiens GN=DAGLA PE=1 SV=3 - [DGLA_HUMAN]
Q9NRH2	SNF-related serine/threonine-protein kinase OS=Homo sapiens GN=SNRK PE=1 SV=2 - [SNRK_HUMAN]
Q9Y6M7	Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=1 SV=2 - [S4A7_HUMAN]
Q9NY46	Sodium channel protein type 3 subunit alpha OS=Homo sapiens GN=SCN3A PE=1 SV=2 - [SCN3A_HUMAN]
Q9UPR5	Sodium/calcium exchanger 2 OS=Homo sapiens GN=SLC8A2 PE=2 SV=2 - [NAC2_HUMAN]
P19634	Sodium/hydrogen exchanger 1 OS=Homo sapiens GN=SLC9A1 PE=1 SV=2 - [SL9A1_HUMAN]
Q5TAH2	Sodium/hydrogen exchanger 11 OS=Homo sapiens GN=SLC9C2 PE=2 SV=1 - [SL9C2_HUMAN]
P48764	Sodium/hydrogen exchanger 3 OS=Homo sapiens GN=SLC9A3 PE=1 SV=2 - [SL9A3_HUMAN]
Q14940	Sodium/hydrogen exchanger 5 OS=Homo sapiens GN=SLC9A5 PE=1 SV=2 - [SL9A5_HUMAN]
P13637	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3 - [AT1A3_HUMAN]
Q9H2J7	Sodium-dependent neutral amino acid transporter B(0)AT2 OS=Homo sapiens GN=SLC6A15 PE=1 SV=1 - [S6A15_HUMAN]
Q96N87	Sodium-dependent neutral amino acid transporter B(0)AT3 OS=Homo sapiens GN=SLC6A18 PE=2 SV=2 - [S6A18_HUMAN]
Q9H2X9	Solute carrier family 12 member 5 OS=Homo sapiens GN=SLC12A5 PE=2 SV=3 - [S12A5_HUMAN]

Q9BXP2	Solute carrier family 12 member 9 OS=Homo sapiens GN=SLC12A9 PE=1 SV=1 - [S12A9_HUMAN]
O95528	Solute carrier family 2, facilitated glucose transporter member 10 OS=Homo sapiens GN=SLC2A10 PE=1 SV=2 - [GTR10_HUMAN]
Q8TD20	Solute carrier family 2, facilitated glucose transporter member 12 OS=Homo sapiens GN=SLC2A12 PE=2 SV=1 - [GTR12_HUMAN]
O15245	Solute carrier family 22 member 1 OS=Homo sapiens GN=SLC22A1 PE=1 SV=2 - [S22A1_HUMAN]
A1A5C7	Solute carrier family 22 member 23 OS=Homo sapiens GN=SLC22A23 PE=1 SV=2 - [S22AN_HUMAN]
Q8IVM8	Solute carrier family 22 member 9 OS=Homo sapiens GN=SLC22A9 PE=1 SV=1 - [S22A9_HUMAN]
Q3KQZ1	Solute carrier family 25 member 35 OS=Homo sapiens GN=SLC25A35 PE=2 SV=1 - [S2535_HUMAN]
Q96H78	Solute carrier family 25 member 44 OS=Homo sapiens GN=SLC25A44 PE=2 SV=1 - [S2544_HUMAN]
Q8NG04	Solute carrier family 26 member 10 OS=Homo sapiens GN=SLC26A10 PE=2 SV=1 - [S2610_HUMAN]
Q9NQQ7	Solute carrier family 35 member C2 OS=Homo sapiens GN=SLC35C2 PE=1 SV=2 - [S35C2_HUMAN]
Q8WV83	Solute carrier family 35 member F5 OS=Homo sapiens GN=SLC35F5 PE=2 SV=1 - [S35F5_HUMAN]
O94956	Solute carrier organic anion transporter family member 2B1 OS=Homo sapiens GN=SLCO2B1 PE=1 SV=2 - [SO2B1_HUMAN]
Q9UIG8	Solute carrier organic anion transporter family member 3A1 OS=Homo sapiens GN=SLCO3A1 PE=1 SV=3 - [SO3A1_HUMAN]
Q9H2Y9	Solute carrier organic anion transporter family member 5A1 OS=Homo sapiens GN=SLCO5A1 PE=2 SV=2 - [SO5A1_HUMAN]
P01241	Somatotropin OS=Homo sapiens GN=GH1 PE=1 SV=2 - [SOMA_HUMAN]
Q07889	Son of sevenless homolog 1 OS=Homo sapiens GN=SOS1 PE=1 SV=1 - [SOS1_HUMAN]
Q9BX66	Sorbin and SH3 domain-containing protein 1 OS=Homo sapiens GN=SORBS1 PE=1 SV=3 - [SRBS1_HUMAN]
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]
Q92673	Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2 - [SORL_HUMAN]
Q9BW04	Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2 - [SARG_HUMAN]
P02549	Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]
P11277	Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5 - [SPTB1_HUMAN]
Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN]
Q9H254	Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens GN=SPTBN4 PE=1 SV=2 - [SPTN4_HUMAN]
Q9NRC6	Spectrin beta chain, non-erythrocytic 5 OS=Homo sapiens GN=SPTBN5 PE=1 SV=2 - [SPTN5_HUMAN]
Q8NFV5	Speedy protein E1 OS=Homo sapiens GN=SPDYE1 PE=2 SV=3 - [SPDE1_HUMAN]
Q5VSR9	Sperm protein associated with the nucleus on the X chromosome N1 OS=Homo sapiens GN=SPANXN1 PE=3 SV=1 - [SPXN1_HUMAN]
Q07617	Sperm-associated antigen 1 OS=Homo sapiens GN=SPAG1 PE=1 SV=3 - [SPAG1_HUMAN]
P09430	Spermatid nuclear transition protein 1 OS=Homo sapiens GN=TNP1 PE=1 SV=2 - [STP1_HUMAN]
Q96SI9	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1 - [STRBP_HUMAN]
Q9BXB7	Spermatogenesis-associated protein 16 OS=Homo sapiens GN=SPATA16 PE=1 SV=3 - [SPT16_HUMAN]
Q8TB22	Spermatogenesis-associated protein 20 OS=Homo sapiens GN=SPATA20 PE=2 SV=3 - [SPT20_HUMAN]
Q5VYP0	Spermatogenesis-associated protein 31A3 OS=Homo sapiens GN=SPATA31A3 PE=2 SV=1 - [S31A3_HUMAN]
Q96LK8	Spermatogenesis-associated protein 32 OS=Homo sapiens GN=SPATA32 PE=1 SV=3 - [SPT32_HUMAN]
Q96N06	Spermatogenesis-associated protein 33 OS=Homo sapiens GN=SPATA33 PE=2 SV=1 - [SPT33_HUMAN]
Q537H7	Spermatogenesis-associated protein 45 OS=Homo sapiens GN=SPATA45 PE=3 SV=1 - [SPT45_HUMAN]
Q9BVQ7	Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2 - [SPA5L_HUMAN]
P28290	Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=1 SV=3 - [SSFA2_HUMAN]
Q9NXE4	Sphingomyelin phosphodiesterase 4 OS=Homo sapiens GN=SMPD4 PE=1 SV=2 - [NSMA3_HUMAN]
O95977	Sphingosine 1-phosphate receptor 4 OS=Homo sapiens GN=S1PR4 PE=1 SV=1 - [S1PR4_HUMAN]
Q9H228	Sphingosine 1-phosphate receptor 5 OS=Homo sapiens GN=S1PR5 PE=2 SV=1 - [S1PR5_HUMAN]
Q8N0Z3	Spindle and centriole-associated protein 1 OS=Homo sapiens GN=SPICE1 PE=1 SV=1 - [SPICE_HUMAN]
Q96BD8	Spindle and kinetochore-associated protein 1 OS=Homo sapiens GN=SKA1 PE=1 SV=1 - [SKA1_HUMAN]
Q6UVJ0	Spindle assembly abnormal protein 6 homolog OS=Homo sapiens GN=SASS6 PE=1 SV=1 - [SAS6_HUMAN]
Q99865	Spindlin-2A OS=Homo sapiens GN=SPIN2A PE=1 SV=3 - [SPI2A_HUMAN]
Q9H7N4	Splicing factor, arginine/serine-rich 19 OS=Homo sapiens GN=SCAF1 PE=1 SV=3 - [SFR19_HUMAN]
Q6ZMY3	SPOC domain-containing protein 1 OS=Homo sapiens GN=SPOCD1 PE=2 SV=1 - [SPOC1_HUMAN]
Q8WW59	SPRY domain-containing protein 4 OS=Homo sapiens GN=SPRYD4 PE=1 SV=2 - [SPRY4_HUMAN]
Q6PJ21	SPRY domain-containing SOCS box protein 3 OS=Homo sapiens GN=SPSB3 PE=1 SV=2 -

	[SPSB3_HUMAN]
Q8WWQ8	Stabilin-2 OS=Homo sapiens GN=STAB2 PE=1 SV=3 - [STAB2_HUMAN]
Q14849	StAR-related lipid transfer protein 3 OS=Homo sapiens GN=STARD3 PE=1 SV=2 - [STAR3_HUMAN]
Q92502	StAR-related lipid transfer protein 8 OS=Homo sapiens GN=STARD8 PE=1 SV=2 - [STAR8_HUMAN]
Q9P2P6	StAR-related lipid transfer protein 9 OS=Homo sapiens GN=STARD9 PE=1 SV=3 - [STAR9_HUMAN]
Q6SZW1	Sterile alpha and TIR motif-containing protein 1 OS=Homo sapiens GN=SARM1 PE=1 SV=1 - [SARM1_HUMAN]
Q8N6K7	Sterile alpha motif domain-containing protein 3 OS=Homo sapiens GN=SAMD3 PE=1 SV=2 - [SAMD3_HUMAN]
Q7Z3H4	Sterile alpha motif domain-containing protein 7 OS=Homo sapiens GN=SAMD7 PE=2 SV=1 - [SAMD7_HUMAN]
Q5K651	Sterile alpha motif domain-containing protein 9 OS=Homo sapiens GN=SAMD9 PE=1 SV=1 - [SAMD9_HUMAN]
P49675	Steroidogenic acute regulatory protein, mitochondrial OS=Homo sapiens GN=STAR PE=1 SV=2 - [STAR_HUMAN]
Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]
Q86WV6	Stimulator of interferon genes protein OS=Homo sapiens GN=TMEM173 PE=1 SV=1 - [STING_HUMAN]
Q9UBI4	Stomatin-like protein 1 OS=Homo sapiens GN=STOML1 PE=1 SV=1 - [STML1_HUMAN]
Q5VSL9	Striatin-interacting protein 1 OS=Homo sapiens GN=STRIP1 PE=1 SV=1 - [STRP1_HUMAN]
Q9UQE7	Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_HUMAN]
Q96SB8	Structural maintenance of chromosomes protein 6 OS=Homo sapiens GN=SMC6 PE=1 SV=2 - [SMC6_HUMAN]
Q9NX18	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Homo sapiens GN=SDHAF2 PE=1 SV=1 - [SDHF2_HUMAN]
Q99643	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Homo sapiens GN=SDHC PE=1 SV=1 - [C560_HUMAN]
P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]
Q9H2B4	Sulfate anion transporter 1 OS=Homo sapiens GN=SLC26A1 PE=1 SV=2 - [S26A1_HUMAN]
O00391	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 - [QSOX1_HUMAN]
P50225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]
Q9UBT2	SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 - [SAE2_HUMAN]
O14544	Suppressor of cytokine signaling 6 OS=Homo sapiens GN=SOCS6 PE=1 SV=2 - [SOCS6_HUMAN]
O75683	Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3 - [SURF6_HUMAN]
Q6UWL2	Sushi domain-containing protein 1 OS=Homo sapiens GN=SUSD1 PE=1 SV=1 - [SUSD1_HUMAN]
O60279	Sushi domain-containing protein 5 OS=Homo sapiens GN=SUSD5 PE=1 SV=3 - [SUSD5_HUMAN]
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 OS=Homo sapiens GN=SMARCAD1 PE=1 SV=2 - [SMRCD_HUMAN]
Q9NZC9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 OS=Homo sapiens GN=SMARCAL1 PE=1 SV=1 - [SMAL1_HUMAN]
A6NDD5	Synapse differentiation-inducing gene protein 1-like OS=Homo sapiens GN=SYNDIG1L PE=3 SV=1 - [SYN1L_HUMAN]
Q8N4V2	Synaptic vesicle 2-related protein OS=Homo sapiens GN=SVOP PE=2 SV=1 - [SVOP_HUMAN]
Q15431	Synaptonemal complex protein 1 OS=Homo sapiens GN=SYCP1 PE=1 SV=2 - [SYCP1_HUMAN]
Q8IZU3	Synaptonemal complex protein 3 OS=Homo sapiens GN=SYCP3 PE=1 SV=1 - [SYCP3_HUMAN]
Q6XYQ8	Synaptotagmin-10 OS=Homo sapiens GN=SYT10 PE=2 SV=1 - [SYT10_HUMAN]
Q9BQS2	Synaptotagmin-15 OS=Homo sapiens GN=SYT15 PE=2 SV=3 - [SYT15_HUMAN]
Q9BSW7	Synaptotagmin-17 OS=Homo sapiens GN=SYT17 PE=1 SV=1 - [SYT17_HUMAN]
Q9HCH5	Synaptotagmin-like protein 2 OS=Homo sapiens GN=SYTL2 PE=1 SV=3 - [SYTL2_HUMAN]
Q9NPQ8	Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3 - [RIC8A_HUMAN]
Q9NX95	Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2 - [SYBU_HUMAN]
Q13277	Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3 - [STX3_HUMAN]
Q5T5C0	Syntaxin-binding protein 5 OS=Homo sapiens GN=STXBP5 PE=1 SV=1 - [STXB5_HUMAN]
Q9UHF0	Tachykinin-3 OS=Homo sapiens GN=TAC3 PE=1 SV=1 - [TKNK_HUMAN]
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]
Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4 - [TLN2_HUMAN]
A7MCY6	TANK-binding kinase 1-binding protein 1 OS=Homo sapiens GN=TBKBP1 PE=1 SV=1 - [TBKB1_HUMAN]
P59541	Taste receptor type 2 member 30 OS=Homo sapiens GN=TAS2R30 PE=2 SV=3 - [T2R30_HUMAN]
P59538	Taste receptor type 2 member 31 OS=Homo sapiens GN=TAS2R31 PE=2 SV=2 - [T2R31_HUMAN]

P59551	Taste receptor type 2 member 60 OS=Homo sapiens GN=TAS2R60 PE=2 SV=1 - [T2R60_HUMAN]
P82094	TATA element modulatory factor OS=Homo sapiens GN=TMF1 PE=1 SV=2 - [TMF1_HUMAN]
O14981	TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2 - [BTAF1_HUMAN]
Q5TCY1	Tau-tubulin kinase 1 OS=Homo sapiens GN=TTBK1 PE=1 SV=2 - [TTBK1_HUMAN]
Q8TEA7	TBC domain-containing protein kinase-like protein OS=Homo sapiens GN=TBCK PE=1 SV=4 - [TBCK_HUMAN]
Q9ULP9	TBC1 domain family member 24 OS=Homo sapiens GN=TBC1D24 PE=1 SV=2 - [TBC24_HUMAN]
Q9UPU7	TBC1 domain family member 2B OS=Homo sapiens GN=TBC1D2B PE=1 SV=2 - [TBD2B_HUMAN]
Q7Z3E1	TCDD-inducible poly [ADP-ribose] polymerase OS=Homo sapiens GN=TIPARP PE=2 SV=1 - [PARPT_HUMAN]
Q8N3R3	T-cell activation inhibitor, mitochondrial OS=Homo sapiens GN=TCAIM PE=2 SV=2 - [TCAIM_HUMAN]
Q8N103	T-cell activation Rho GTPase-activating protein OS=Homo sapiens GN=TAGAP PE=1 SV=1 - [TAGAP_HUMAN]
P06729	T-cell surface antigen CD2 OS=Homo sapiens GN=CD2 PE=1 SV=2 - [CD2_HUMAN]
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]
Q5JU00	T-complex-associated testis-expressed protein 1 OS=Homo sapiens GN=TCTE1 PE=2 SV=1 - [TCTE1_HUMAN]
Q6ZSZ6	Teashirt homolog 1 OS=Homo sapiens GN=TSHZ1 PE=2 SV=2 - [TSH1_HUMAN]
Q63HK5	Teashirt homolog 3 OS=Homo sapiens GN=TSHZ3 PE=1 SV=2 - [TSH3_HUMAN]
Q7Z6L1	Tectonin beta-propeller repeat-containing protein 1 OS=Homo sapiens GN=TECPR1 PE=1 SV=1 - [TCPR1_HUMAN]
Q86US8	Telomerase-binding protein EST1A OS=Homo sapiens GN=SMG6 PE=1 SV=2 - [EST1A_HUMAN]
Q6N022	Teneurin-4 OS=Homo sapiens GN=TENM4 PE=1 SV=2 - [TEN4_HUMAN]
Q68CZ2	Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2 - [TENS3_HUMAN]
Q5TAX3	Terminal uridylyltransferase 4 OS=Homo sapiens GN=ZCCHC11 PE=1 SV=3 - [TUT4_HUMAN]
Q9BXT5	Testis-expressed sequence 15 protein OS=Homo sapiens GN=TEX15 PE=2 SV=2 - [TEX15_HUMAN]
Q8IWB9	Testis-expressed sequence 2 protein OS=Homo sapiens GN=TEX2 PE=1 SV=2 - [TEX2_HUMAN]
Q9BZW7	Testis-specific gene 10 protein OS=Homo sapiens GN=TSGA10 PE=1 SV=1 - [TSG10_HUMAN]
Q9BXA7	Testis-specific serine/threonine-protein kinase 1 OS=Homo sapiens GN=TSSK1B PE=1 SV=1 - [TSSK1_HUMAN]
Q9BZE9	Tether containing UBX domain for GLUT4 OS=Homo sapiens GN=ASPSCR1 PE=1 SV=1 - [ASPC1_HUMAN]
Q9UKR8	Tetraspanin-16 OS=Homo sapiens GN=TSPAN16 PE=2 SV=1 - [TSN16_HUMAN]
Q8NEE8	Tetratricopeptide repeat protein 16 OS=Homo sapiens GN=TTC16 PE=2 SV=2 - [TTC16_HUMAN]
Q8NDW8	Tetratricopeptide repeat protein 21A OS=Homo sapiens GN=TTC21A PE=2 SV=3 - [TT21A_HUMAN]
Q7Z4L5	Tetratricopeptide repeat protein 21B OS=Homo sapiens GN=TTC21B PE=1 SV=2 - [TT21B_HUMAN]
Q96AY4	Tetratricopeptide repeat protein 28 OS=Homo sapiens GN=TTC28 PE=1 SV=4 - [TTC28_HUMAN]
A8MYJ7	Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2 - [TTC34_HUMAN]
Q5R3I4	Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38 PE=1 SV=1 - [TTC38_HUMAN]
Q8N0Z6	Tetratricopeptide repeat protein 5 OS=Homo sapiens GN=TTC5 PE=1 SV=2 - [TTC5_HUMAN]
Q8TAM2	Tetratricopeptide repeat protein 8 OS=Homo sapiens GN=TTC8 PE=1 SV=2 - [TTC8_HUMAN]
O95411	TGFB1-induced anti-apoptotic factor 1 OS=Homo sapiens GN=TIAF1 PE=2 SV=2 - [TIAF1_HUMAN]
P36897	TGF-beta receptor type-1 OS=Homo sapiens GN=TGFBR1 PE=1 SV=1 - [TGFR1_HUMAN]
Q8WTV1	THAP domain-containing protein 3 OS=Homo sapiens GN=THAP3 PE=1 SV=1 - [THAP3_HUMAN]
Q8WY91	THAP domain-containing protein 4 OS=Homo sapiens GN=THAP4 PE=1 SV=2 - [THAP4_HUMAN]
Q96J42	Thioredoxin domain-containing protein 15 OS=Homo sapiens GN=TXNDC15 PE=1 SV=1 - [TXD15_HUMAN]
Q9P2K2	Thioredoxin domain-containing protein 16 OS=Homo sapiens GN=TXNDC16 PE=2 SV=4 - [TXD16_HUMAN]
Q9H3M7	Thioredoxin-interacting protein OS=Homo sapiens GN=TXNIP PE=1 SV=1 - [TXNIP_HUMAN]
Q8NI27	THO complex subunit 2 OS=Homo sapiens GN=THOC2 PE=1 SV=2 - [THOC2_HUMAN]
P26639	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3 - [SYTC_HUMAN]
P40225	Thrombopoietin OS=Homo sapiens GN=THPO PE=1 SV=1 - [TPO_HUMAN]
P21731	Thromboxane A2 receptor OS=Homo sapiens GN=TBXA2R PE=1 SV=3 - [TA2R_HUMAN]
Q9BV44	THUMP domain-containing protein 3 OS=Homo sapiens GN=THUMPD3 PE=1 SV=1 - [THUM3_HUMAN]
O00142	Thymidine kinase 2, mitochondrial OS=Homo sapiens GN=TK2 PE=1 SV=4 - [KITM_HUMAN]
P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]

Q6YHU6	Thyroid adenoma-associated protein OS=Homo sapiens GN=THADA PE=1 SV=1 - [THADA_HUMAN]
Q96MW7	Tigger transposable element-derived protein 1 OS=Homo sapiens GN=TIGD1 PE=1 SV=1 - [TIGD1_HUMAN]
Q8IY51	Tigger transposable element-derived protein 4 OS=Homo sapiens GN=TIGD4 PE=2 SV=2 - [TIGD4_HUMAN]
Q07157	Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3 - [ZO1_HUMAN]
Q9UDY2	Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2 - [ZO2_HUMAN]
O95049	Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=1 SV=3 - [ZO3_HUMAN]
Q8WZ42	Titin OS=Homo sapiens GN=TTN PE=1 SV=4 - [TITIN_HUMAN]
Q6P9B6	TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=2 - [TLDC1_HUMAN]
Q96KP6	TNFAIP3-interacting protein 3 OS=Homo sapiens GN=TNIP3 PE=1 SV=2 - [TNIP3_HUMAN]
Q15399	Toll-like receptor 1 OS=Homo sapiens GN=TLR1 PE=1 SV=3 - [TLR1_HUMAN]
Q9BXR5	Toll-like receptor 10 OS=Homo sapiens GN=TLR10 PE=1 SV=2 - [TLR10_HUMAN]
Q9Y2C9	Toll-like receptor 6 OS=Homo sapiens GN=TLR6 PE=1 SV=2 - [TLR6_HUMAN]
Q96HA7	Tonsoku-like protein OS=Homo sapiens GN=TONSL PE=1 SV=2 - [TONSL_HUMAN]
Q96RI8	Trace amine-associated receptor 6 OS=Homo sapiens GN=TAAR6 PE=2 SV=1 - [TAAR6_HUMAN]
Q9Y228	TRAF3-interacting JNK-activating modulator OS=Homo sapiens GN=TRAF3IP3 PE=1 SV=2 - [T3JAM_HUMAN]
P48553	Trafficking protein particle complex subunit 10 OS=Homo sapiens GN=TRAPPC10 PE=1 SV=2 - [TPC10_HUMAN]
Q7Z392	Trafficking protein particle complex subunit 11 OS=Homo sapiens GN=TRAPPC11 PE=1 SV=2 - [TPC11_HUMAN]
Q8WVT3	Trafficking protein particle complex subunit 12 OS=Homo sapiens GN=TRAPPC12 PE=1 SV=3 - [TPC12_HUMAN]
Q9Y2L5	Trafficking protein particle complex subunit 8 OS=Homo sapiens GN=TRAPPC8 PE=1 SV=2 - [TPPC8_HUMAN]
Q96EI5	Transcription elongation factor A protein-like 4 OS=Homo sapiens GN=TCEAL4 PE=1 SV=2 - [TCAL4_HUMAN]
O14776	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2 - [TCRG1_HUMAN]
Q9UGU0	Transcription factor 20 OS=Homo sapiens GN=TCF20 PE=1 SV=3 - [TCF20_HUMAN]
Q7RTU1	Transcription factor 23 OS=Homo sapiens GN=TCF23 PE=2 SV=1 - [TCF23_HUMAN]
Q00059	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM_HUMAN]
O75461	Transcription factor E2F6 OS=Homo sapiens GN=E2F6 PE=1 SV=1 - [E2F6_HUMAN]
Q96AV8	Transcription factor E2F7 OS=Homo sapiens GN=E2F7 PE=1 SV=3 - [E2F7_HUMAN]
Q9HCC6	Transcription factor HES-4 OS=Homo sapiens GN=HES4 PE=2 SV=1 - [HES4_HUMAN]
Q5T1R4	Transcription factor HIVEP3 OS=Homo sapiens GN=HIVEP3 PE=2 SV=1 - [ZEP3_HUMAN]
P48380	Transcription factor RFX3 OS=Homo sapiens GN=RFX3 PE=1 SV=2 - [RFX3_HUMAN]
O94993	Transcription factor SOX-30 OS=Homo sapiens GN=SOX30 PE=1 SV=1 - [SOX30_HUMAN]
P35711	Transcription factor SOX-5 OS=Homo sapiens GN=SOX5 PE=1 SV=3 - [SOX5_HUMAN]
P08047	Transcription factor Sp1 OS=Homo sapiens GN=SP1 PE=1 SV=3 - [SP1_HUMAN]
A6H8Y1	Transcription factor TFIIIB component B'' homolog OS=Homo sapiens GN=BDP1 PE=1 SV=3 - [BDP1_HUMAN]
Q12962	Transcription initiation factor TFIID subunit 10 OS=Homo sapiens GN=TAF10 PE=1 SV=1 - [TAF10_HUMAN]
O15164	Transcription intermediary factor 1-alpha OS=Homo sapiens GN=TRIM24 PE=1 SV=3 - [TIF1A_HUMAN]
Q49AM1	Transcription termination factor 2, mitochondrial OS=Homo sapiens GN=MTERF2 PE=1 SV=2 - [MTEF2_HUMAN]
Q86TJ2	Transcriptional adapter 2-beta OS=Homo sapiens GN=TADA2B PE=1 SV=2 - [TAD2B_HUMAN]
Q15562	Transcriptional enhancer factor TEF-4 OS=Homo sapiens GN=TEAD2 PE=1 SV=2 - [TEAD2_HUMAN]
Q04724	Transducin-like enhancer protein 1 OS=Homo sapiens GN=TLE1 PE=1 SV=2 - [TLE1_HUMAN]
Q04726	Transducin-like enhancer protein 3 OS=Homo sapiens GN=TLE3 PE=1 SV=2 - [TLE3_HUMAN]
Q9Y4A5	Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3 - [TRRAP_HUMAN]
Q13595	Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1 - [TRA2A_HUMAN]
Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]
O94759	Transient receptor potential cation channel subfamily M member 2 OS=Homo sapiens GN=TRPM2 PE=1 SV=2 - [TRPM2_HUMAN]
Q8TD43	Transient receptor potential cation channel subfamily M member 4 OS=Homo sapiens GN=TRPM4 PE=1 SV=1 - [TRPM4_HUMAN]
Q7Z2W7	Transient receptor potential cation channel subfamily M member 8 OS=Homo sapiens GN=TRPM8 PE=1 SV=2 - [TRPM8_HUMAN]
Q8NET8	Transient receptor potential cation channel subfamily V member 3 OS=Homo sapiens GN=TRPV3 PE=1 SV=2 - [TRPV3_HUMAN]

P51854	Transketolase-like protein 1 OS=Homo sapiens GN=TKTL1 PE=1 SV=2 - [TKTL1_HUMAN]
P46199	Translation initiation factor IF-2, mitochondrial OS=Homo sapiens GN=MTIF2 PE=1 SV=2 - [IF2M_HUMAN]
Q8N609	Translocating chain-associated membrane protein 1-like 1 OS=Homo sapiens GN=TRAM1L1 PE=2 SV=2 - [TR1L1_HUMAN]
Q8N6Q1	Transmembrane and coiled-coil domain-containing protein 5A OS=Homo sapiens GN=TMCO5A PE=2 SV=2 - [TMC5A_HUMAN]
O75069	Transmembrane and coiled-coil domains protein 2 OS=Homo sapiens GN=TMCC2 PE=1 SV=3 - [TMCC2_HUMAN]
Q6NXT6	Transmembrane anterior posterior transformation protein 1 homolog OS=Homo sapiens GN=TAPT1 PE=1 SV=1 - [TAPT1_HUMAN]
Q8IU68	Transmembrane channel-like protein 8 OS=Homo sapiens GN=TMC8 PE=1 SV=1 - [TMC8_HUMAN]
Q9BZD6	Transmembrane gamma-carboxyglutamic acid protein 4 OS=Homo sapiens GN=PRRG4 PE=1 SV=1 - [TMG4_HUMAN]
Q6ZMR5	Transmembrane protease serine 11A OS=Homo sapiens GN=TMPRSS11A PE=1 SV=1 - [TM11A_HUMAN]
Q86WS5	Transmembrane protease serine 12 OS=Homo sapiens GN=TMPRSS12 PE=1 SV=2 - [TMPSC_HUMAN]
Q9BYE2	Transmembrane protease serine 13 OS=Homo sapiens GN=TMPRSS13 PE=2 SV=4 - [TMPSD_HUMAN]
P57727	Transmembrane protease serine 3 OS=Homo sapiens GN=TMPRSS3 PE=1 SV=2 - [TMPS3_HUMAN]
Q96IK0	Transmembrane protein 101 OS=Homo sapiens GN=TMEM101 PE=1 SV=1 - [TM101_HUMAN]
Q9BVC6	Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1 - [TM109_HUMAN]
Q86TL2	Transmembrane protein 110 OS=Homo sapiens GN=TMEM110 PE=2 SV=1 - [TM110_HUMAN]
Q96AN5	Transmembrane protein 143 OS=Homo sapiens GN=TMEM143 PE=2 SV=1 - [TM143_HUMAN]
Q8N614	Transmembrane protein 156 OS=Homo sapiens GN=TMEM156 PE=2 SV=2 - [TM156_HUMAN]
Q9H0V1	Transmembrane protein 168 OS=Homo sapiens GN=TMEM168 PE=2 SV=2 - [TM168_HUMAN]
Q96HH4	Transmembrane protein 169 OS=Homo sapiens GN=TMEM169 PE=2 SV=1 - [TM169_HUMAN]
Q9BSA9	Transmembrane protein 175 OS=Homo sapiens GN=TMEM175 PE=1 SV=1 - [TM175_HUMAN]
Q9H0A3	Transmembrane protein 191A OS=Homo sapiens GN=TMEM191A PE=2 SV=1 - [T191A_HUMAN]
Q69YZ2	Transmembrane protein 200B OS=Homo sapiens GN=TMEM200B PE=2 SV=1 - [T200B_HUMAN]
Q9H6L2	Transmembrane protein 231 OS=Homo sapiens GN=TMEM231 PE=1 SV=1 - [TM231_HUMAN]
C9JQI7	Transmembrane protein 232 OS=Homo sapiens GN=TMEM232 PE=2 SV=2 - [TM232_HUMAN]
Q9NWH2	Transmembrane protein 242 OS=Homo sapiens GN=TMEM242 PE=1 SV=1 - [TM242_HUMAN]
Q9BRR3	Transmembrane protein 246 OS=Homo sapiens GN=TMEM246 PE=1 SV=1 - [TM246_HUMAN]
Q2WGJ8	Transmembrane protein 249 OS=Homo sapiens GN=TMEM249 PE=2 SV=1 - [TM249_HUMAN]
Q96HV5	Transmembrane protein 41A OS=Homo sapiens GN=TMEM41A PE=1 SV=1 - [TM41A_HUMAN]
Q6P2H8	Transmembrane protein 53 OS=Homo sapiens GN=TMEM53 PE=2 SV=1 - [TMM53_HUMAN]
Q0P6H9	Transmembrane protein 62 OS=Homo sapiens GN=TMEM62 PE=1 SV=1 - [TMM62_HUMAN]
Q9BSE2	Transmembrane protein 79 OS=Homo sapiens GN=TMEM79 PE=1 SV=1 - [TMM79_HUMAN]
Q9P0T7	Transmembrane protein 9 OS=Homo sapiens GN=TMEM9 PE=1 SV=1 - [TMEM9_HUMAN]
Q2M3C6	Transmembrane protein C15orf27 OS=Homo sapiens GN=C15orf27 PE=2 SV=2 - [CO027_HUMAN]
O75949	Transmembrane protein FAM155B OS=Homo sapiens GN=FAM155B PE=2 SV=2 - [F155B_HUMAN]
Q13428	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN]
Q13061	Triadin OS=Homo sapiens GN=TRDN PE=1 SV=4 - [TRDN_HUMAN]
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]
Q9H2D6	TRIO and F-actin-binding protein OS=Homo sapiens GN=TRIOBP PE=1 SV=3 - [TARA_HUMAN]
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 - [TPIS_HUMAN]
Q9C040	Tripartite motif-containing protein 2 OS=Homo sapiens GN=TRIM2 PE=1 SV=1 - [TRIM2_HUMAN]
Q14134	Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2 - [TRI29_HUMAN]
O75382	Tripartite motif-containing protein 3 OS=Homo sapiens GN=TRIM3 PE=1 SV=2 - [TRIM3_HUMAN]
Q9UPQ4	Tripartite motif-containing protein 35 OS=Homo sapiens GN=TRIM35 PE=1 SV=2 - [TRI35_HUMAN]
O15016	Tripartite motif-containing protein 66 OS=Homo sapiens GN=TRIM66 PE=2 SV=4 - [TRI66_HUMAN]
Q9C029	Tripartite motif-containing protein 7 OS=Homo sapiens GN=TRIM7 PE=1 SV=2 - [TRIM7_HUMAN]
O14773	Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2 - [TPP1_HUMAN]
Q9UBP6	tRNA (guanine-N(7)-)-methyltransferase OS=Homo sapiens GN=METTL1 PE=1 SV=1 - [TRMB_HUMAN]
Q6PF06	tRNA methyltransferase 10 homolog B OS=Homo sapiens GN=TRMT10B PE=2 SV=1 - [TM10B_HUMAN]
Q969Y2	tRNA modification GTPase GTPBP3, mitochondrial OS=Homo sapiens GN=GTPBP3 PE=1 SV=2 - [GTPB3_HUMAN]

Q9NX74	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like OS=Homo sapiens GN=DUS2 PE=1 SV=1 - [DUS2L_HUMAN]
Q9BSV6	tRNA-splicing endonuclease subunit Sen34 OS=Homo sapiens GN=TSEN34 PE=1 SV=1 - [SEN34_HUMAN]
Q9NZQ9	Tropomodulin-4 OS=Homo sapiens GN=TMOD4 PE=2 SV=1 - [TMOD4_HUMAN]
Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]
Q9UGM6	Tryptophan--tRNA ligase, mitochondrial OS=Homo sapiens GN=WARS2 PE=1 SV=1 - [SYWM_HUMAN]
Q9Y3Q8	TSC22 domain family protein 4 OS=Homo sapiens GN=TSC22D4 PE=1 SV=2 - [T22D4_HUMAN]
Q9NRJ4	Tubby-related protein 4 OS=Homo sapiens GN=TULP4 PE=2 SV=2 - [TULP4_HUMAN]
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]
Q6ZTW0	Tubulin polyglutamylase complex subunit 1 OS=Homo sapiens GN=TPGS1 PE=2 SV=2 - [TPGS1_HUMAN]
A6NNM8	Tubulin polyglutamylase TTLL13P OS=Homo sapiens GN=TTLL13P PE=2 SV=2 - [TTL13_HUMAN]
Q6ZT98	Tubulin polyglutamylase TTLL7 OS=Homo sapiens GN=TTLL7 PE=2 SV=2 - [TTLL7_HUMAN]
Q5VZ19	Tudor domain-containing protein 10 OS=Homo sapiens GN=TDRD10 PE=2 SV=3 - [TDR10_HUMAN]
Q8NAT2	Tudor domain-containing protein 5 OS=Homo sapiens GN=TDRD5 PE=1 SV=3 - [TDRD5_HUMAN]
Q8NHU6	Tudor domain-containing protein 7 OS=Homo sapiens GN=TDRD7 PE=1 SV=2 - [TDRD7_HUMAN]
Q9UBB9	Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=1 SV=1 - [TFP11_HUMAN]
Q5GJ75	Tumor necrosis factor alpha-induced protein 8-like protein 3 OS=Homo sapiens GN=TNFAIP8L3 PE=1 SV=1 - [TP8L3_HUMAN]
Q969Z4	Tumor necrosis factor receptor superfamily member 19L OS=Homo sapiens GN=RELT PE=1 SV=1 - [TR19L_HUMAN]
O75509	Tumor necrosis factor receptor superfamily member 21 OS=Homo sapiens GN=TNFRSF21 PE=1 SV=1 - [TNR21_HUMAN]
Q16890	Tumor protein D53 OS=Homo sapiens GN=TPD52L1 PE=1 SV=1 - [TPD53_HUMAN]
O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]
Q8NHX9	Two pore calcium channel protein 2 OS=Homo sapiens GN=TPCN2 PE=1 SV=2 - [TPC2_HUMAN]
Q96PE3	Type I inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4A PE=1 SV=1 - [INP4A_HUMAN]
O15327	Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4 - [INP4B_HUMAN]
P30556	Type-1 angiotensin II receptor OS=Homo sapiens GN=AGTR1 PE=1 SV=1 - [AGTR1_HUMAN]
P50052	Type-2 angiotensin II receptor OS=Homo sapiens GN=AGTR2 PE=1 SV=1 - [AGTR2_HUMAN]
P17735	Tyrosine aminotransferase OS=Homo sapiens GN=TAT PE=1 SV=1 - [ATTY_HUMAN]
Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2 - [BAZ1B_HUMAN]
P16591	Tyrosine-protein kinase Fer OS=Homo sapiens GN=FER PE=1 SV=2 - [FER_HUMAN]
P09769	Tyrosine-protein kinase Fgr OS=Homo sapiens GN=FGR PE=1 SV=2 - [FGR_HUMAN]
O60674	Tyrosine-protein kinase JAK2 OS=Homo sapiens GN=JAK2 PE=1 SV=2 - [JAK2_HUMAN]
P07948	Tyrosine-protein kinase Lyn OS=Homo sapiens GN=LYN PE=1 SV=3 - [LYN_HUMAN]
P35590	Tyrosine-protein kinase receptor Tie-1 OS=Homo sapiens GN=TIE1 PE=1 SV=1 - [TIE1_HUMAN]
Q06418	Tyrosine-protein kinase receptor TYRO3 OS=Homo sapiens GN=TYRO3 PE=1 SV=1 - [TYRO3_HUMAN]
Q6J9G0	Tyrosine-protein kinase STYK1 OS=Homo sapiens GN=STYK1 PE=1 SV=4 - [STYK1_HUMAN]
Q01973	Tyrosine-protein kinase transmembrane receptor ROR1 OS=Homo sapiens GN=ROR1 PE=1 SV=2 - [ROR1_HUMAN]
P07947	Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3 - [YES_HUMAN]
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 - [PTN1_HUMAN]
P29074	Tyrosine-protein phosphatase non-receptor type 4 OS=Homo sapiens GN=PTPN4 PE=1 SV=1 - [PTN4_HUMAN]
P43378	Tyrosine-protein phosphatase non-receptor type 9 OS=Homo sapiens GN=PTPN9 PE=1 SV=1 - [PTN9_HUMAN]
P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4 - [SYYC_HUMAN]
O15042	U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2 - [SR140_HUMAN]
O00566	U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2 - [MPP10_HUMAN]
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1 - [UT14A_HUMAN]
O43818	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1 - [U3IP2_HUMAN]
O43290	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 - [SNUT1_HUMAN]
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 -

	[U520_HUMAN]
P83369	U7 snRNA-associated Sm-like protein LSm11 OS=Homo sapiens GN=LSM11 PE=1 SV=2 - [LSM11_HUMAN]
Q6ZU65	Ubinuclein-2 OS=Homo sapiens GN=UBN2 PE=1 SV=2 - [UBN2_HUMAN]
Q9UMX0	Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2 - [UBQL1_HUMAN]
Q9NRR5	Ubiquilin-4 OS=Homo sapiens GN=UBQLN4 PE=1 SV=2 - [UBQL4_HUMAN]
A6NCW0	Ubiquitin carboxyl-terminal hydrolase 17-like protein 3 OS=Homo sapiens GN=USP17L3 PE=3 SV=1 - [U17L3_HUMAN]
Q9Y2K6	Ubiquitin carboxyl-terminal hydrolase 20 OS=Homo sapiens GN=USP20 PE=1 SV=2 - [UBP20_HUMAN]
Q9BXU7	Ubiquitin carboxyl-terminal hydrolase 26 OS=Homo sapiens GN=USP26 PE=1 SV=1 - [UBP26_HUMAN]
Q70CQ4	Ubiquitin carboxyl-terminal hydrolase 31 OS=Homo sapiens GN=USP31 PE=2 SV=2 - [UBP31_HUMAN]
Q9P2H5	Ubiquitin carboxyl-terminal hydrolase 35 OS=Homo sapiens GN=USP35 PE=1 SV=3 - [UBP35_HUMAN]
Q9P275	Ubiquitin carboxyl-terminal hydrolase 36 OS=Homo sapiens GN=USP36 PE=1 SV=3 - [UBP36_HUMAN]
Q86T82	Ubiquitin carboxyl-terminal hydrolase 37 OS=Homo sapiens GN=USP37 PE=1 SV=2 - [UBP37_HUMAN]
Q70EL4	Ubiquitin carboxyl-terminal hydrolase 43 OS=Homo sapiens GN=USP43 PE=1 SV=2 - [UBP43_HUMAN]
P35125	Ubiquitin carboxyl-terminal hydrolase 6 OS=Homo sapiens GN=USP6 PE=1 SV=2 - [UBP6_HUMAN]
Q9HAC8	Ubiquitin domain-containing protein 1 OS=Homo sapiens GN=UBTD1 PE=1 SV=1 - [UBTD1_HUMAN]
O14562	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=1 SV=2 - [UBFD1_HUMAN]
Q96BN8	Ubiquitin thioesterase otulin OS=Homo sapiens GN=OTULIN PE=1 SV=3 - [OTUL_HUMAN]
P57075	Ubiquitin-associated and SH3 domain-containing protein A OS=Homo sapiens GN=UBASH3A PE=1 SV=1 - [UBS3A_HUMAN]
Q8TF42	Ubiquitin-associated and SH3 domain-containing protein B OS=Homo sapiens GN=UBASH3B PE=1 SV=2 - [UBS3B_HUMAN]
Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1 - [UBAC1_HUMAN]
O00762	Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1 - [UBE2C_HUMAN]
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 - [UBA1_HUMAN]
P05161	Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 - [ISG15_HUMAN]
Q7Z3V4	Ubiquitin-protein ligase E3B OS=Homo sapiens GN=UBE3B PE=1 SV=3 - [UBE3B_HUMAN]
P78381	UDP-galactose translocator OS=Homo sapiens GN=SLC35A2 PE=1 SV=1 - [S35A2_HUMAN]
O75752	UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 1 OS=Homo sapiens GN=B3GALNT1 PE=2 SV=1 - [B3GL1_HUMAN]
O60701	UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 - [UGDH_HUMAN]
Q9NYU1	UDP-glucose:glycoprotein glucosyltransferase 2 OS=Homo sapiens GN=UGGT2 PE=1 SV=4 - [UGGG2_HUMAN]
P54855	UDP-glucuronosyltransferase 2B15 OS=Homo sapiens GN=UGT2B15 PE=1 SV=3 - [UDB15_HUMAN]
P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3 - [OGT1_HUMAN]
Q5EBM0	UMP-CMP kinase 2, mitochondrial OS=Homo sapiens GN=CMPK2 PE=1 SV=3 - [CMPK2_HUMAN]
Q3MIX3	Uncharacterized aarF domain-containing protein kinase 5 OS=Homo sapiens GN=ADCK5 PE=1 SV=2 - [ADCK5_HUMAN]
Q8N7S6	Uncharacterized protein ARIH2OS OS=Homo sapiens GN=ARIH2OS PE=2 SV=1 - [ARI2O_HUMAN]
Q8N655	Uncharacterized protein C10orf12 OS=Homo sapiens GN=C10orf12 PE=1 SV=1 - [CJ012_HUMAN]
Q9H943	Uncharacterized protein C10orf68 OS=Homo sapiens GN=C10orf68 PE=2 SV=2 - [CJ068_HUMAN]
Q6ZUT1	Uncharacterized protein C11orf57 OS=Homo sapiens GN=C11orf57 PE=1 SV=2 - [CK057_HUMAN]
C9JLR9	Uncharacterized protein C11orf95 OS=Homo sapiens GN=C11orf95 PE=2 SV=1 - [CK095_HUMAN]
Q7Z7L8	Uncharacterized protein C11orf96 OS=Homo sapiens GN=C11orf96 PE=1 SV=3 - [CK096_HUMAN]
Q96C57	Uncharacterized protein C12orf43 OS=Homo sapiens GN=C12orf43 PE=1 SV=2 - [CL043_HUMAN]
Q86SX3	Uncharacterized protein C14orf80 OS=Homo sapiens GN=C14orf80 PE=2 SV=2 - [CN080_HUMAN]
A8K5M9	Uncharacterized protein C15orf62, mitochondrial OS=Homo sapiens GN=C15orf62 PE=2 SV=1 - [CO062_HUMAN]
Q96LL3	Uncharacterized protein C16orf92 OS=Homo sapiens GN=C16orf92 PE=2 SV=1 - [CP092_HUMAN]
F2Z3M2	Uncharacterized protein C17orf112 OS=Homo sapiens GN=C17orf112 PE=4 SV=1 - [CQ112_HUMAN]
Q5SNV9	Uncharacterized protein C1orf167 OS=Homo sapiens GN=C1orf167 PE=2 SV=2 - [CA167_HUMAN]
Q5TEA3	Uncharacterized protein C20orf194 OS=Homo sapiens GN=C20orf194 PE=1 SV=1 - [CT194_HUMAN]
Q08AI8	Uncharacterized protein C2orf54 OS=Homo sapiens GN=C2orf54 PE=2 SV=2 - [CB054_HUMAN]
A6NGG8	Uncharacterized protein C2orf71 OS=Homo sapiens GN=C2orf71 PE=1 SV=1 - [CB071_HUMAN]

A6NCS6	Uncharacterized protein C2orf72 OS=Homo sapiens GN=C2orf72 PE=1 SV=2 - [CB072_HUMAN]
Q8ND61	Uncharacterized protein C3orf20 OS=Homo sapiens GN=C3orf20 PE=2 SV=2 - [CC020_HUMAN]
Q96MH7	Uncharacterized protein C5orf34 OS=Homo sapiens GN=C5orf34 PE=2 SV=2 - [CE034_HUMAN]
Q5T5N4	Uncharacterized protein C6orf118 OS=Homo sapiens GN=C6orf118 PE=2 SV=1 - [CF118_HUMAN]
Q5T0Z8	Uncharacterized protein C6orf132 OS=Homo sapiens GN=C6orf132 PE=1 SV=4 - [CF132_HUMAN]
Q5TEZ5	Uncharacterized protein C6orf163 OS=Homo sapiens GN=C6orf163 PE=4 SV=2 - [CF163_HUMAN]
P0C671	Uncharacterized protein C6orf222 OS=Homo sapiens GN=C6orf222 PE=1 SV=1 - [CF222_HUMAN]
Q6ZTR5	Uncharacterized protein CXorf22 OS=Homo sapiens GN=CXorf22 PE=2 SV=3 - [CX022_HUMAN]
Q9UF83	Uncharacterized protein DKFZp434B061 OS=Homo sapiens PE=2 SV=2 - [YM012_HUMAN]
Q8N2X6	Uncharacterized protein EXOC3-AS1 OS=Homo sapiens GN=EXOC3-AS1 PE=1 SV=1 - [EXAS1_HUMAN]
O15063	Uncharacterized protein KIAA0355 OS=Homo sapiens GN=KIAA0355 PE=1 SV=2 - [K0355_HUMAN]
Q68EN5	Uncharacterized protein KIAA0895-like OS=Homo sapiens GN=KIAA0895L PE=2 SV=1 - [K895L_HUMAN]
Q2LD37	Uncharacterized protein KIAA1109 OS=Homo sapiens GN=KIAA1109 PE=1 SV=2 - [K1109_HUMAN]
Q9ULL0	Uncharacterized protein KIAA1210 OS=Homo sapiens GN=KIAA1210 PE=2 SV=3 - [K1210_HUMAN]
Q6NV74	Uncharacterized protein KIAA1211-like OS=Homo sapiens GN=KIAA1211L PE=2 SV=3 - [K121L_HUMAN]
Q9HCM1	Uncharacterized protein KIAA1551 OS=Homo sapiens GN=KIAA1551 PE=1 SV=3 - [K1551_HUMAN]
Q0VF49	Uncharacterized protein KIAA2012 OS=Homo sapiens GN=KIAA2012 PE=2 SV=2 - [K2012_HUMAN]
Q5HYC2	Uncharacterized protein KIAA2026 OS=Homo sapiens GN=KIAA2026 PE=2 SV=2 - [K2026_HUMAN]
Q96FF7	Uncharacterized protein LOC113230 OS=Homo sapiens PE=2 SV=4 - [YS003_HUMAN]
Q8NCS4	Uncharacterized protein ZMYM6NB OS=Homo sapiens GN=ZMYM6NB PE=2 SV=1 - [ZMYNB_HUMAN]
Q9UBC5	Unconventional myosin-Ia OS=Homo sapiens GN=MYO1A PE=1 SV=1 - [MYO1A_HUMAN]
O43795	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 - [MYO1B_HUMAN]
O94832	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN]
O00160	Unconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 - [MYO1F_HUMAN]
B2RTY4	Unconventional myosin-IXa OS=Homo sapiens GN=MYO9A PE=1 SV=2 - [MYO9A_HUMAN]
Q13459	Unconventional myosin-IXb OS=Homo sapiens GN=MYO9B PE=1 SV=3 - [MYO9B_HUMAN]
Q9Y4I1	Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=1 SV=2 - [MYO5A_HUMAN]
Q9UM54	Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4 - [MYO6_HUMAN]
Q6PIF6	Unconventional myosin-VIIb OS=Homo sapiens GN=MYO7B PE=1 SV=2 - [MYO7B_HUMAN]
Q9UKN7	Unconventional myosin-XV OS=Homo sapiens GN=MYO15A PE=1 SV=2 - [MYO15_HUMAN]
Q96JP2	Unconventional myosin-XVB OS=Homo sapiens GN=MYO15B PE=1 SV=2 - [MY15B_HUMAN]
Q8IUG5	Unconventional myosin-XVIIIb OS=Homo sapiens GN=MYO18B PE=1 SV=1 - [MY18B_HUMAN]
Q9BZE7	UPF0193 protein EVG1 OS=Homo sapiens GN=C22orf23 PE=1 SV=1 - [EVG1_HUMAN]
Q9BPX7	UPF0415 protein C7orf25 OS=Homo sapiens GN=C7orf25 PE=1 SV=1 - [CG025_HUMAN]
Q49AR2	UPF0489 protein C5orf22 OS=Homo sapiens GN=C5orf22 PE=1 SV=2 - [CE022_HUMAN]
Q8N8R5	UPF0565 protein C2orf69 OS=Homo sapiens GN=C2orf69 PE=1 SV=1 - [CB069_HUMAN]
A8MWY0	UPF0577 protein KIAA1324-like OS=Homo sapiens GN=KIAA1324L PE=2 SV=2 - [K132L_HUMAN]
Q92738	USP6 N-terminal-like protein OS=Homo sapiens GN=USP6NL PE=1 SV=3 - [US6NL_HUMAN]
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]
P46939	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 - [UTRO_HUMAN]
Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=1 SV=2 - [UACA_HUMAN]
P15918	V(D)J recombination-activating protein 1 OS=Homo sapiens GN=RAG1 PE=1 SV=2 - [RAG1_HUMAN]
Q7Z7G8	Vacuolar protein sorting-associated protein 13B OS=Homo sapiens GN=VPS13B PE=1 SV=2 - [VP13B_HUMAN]
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1 - [VP13C_HUMAN]
Q9H269	Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=1 SV=2 - [VPS16_HUMAN]
Q9NRW7	Vacuolar protein sorting-associated protein 45 OS=Homo sapiens GN=VPS45 PE=1 SV=1 - [VPS45_HUMAN]
Q15906	Vacuolar protein sorting-associated protein 72 homolog OS=Homo sapiens GN=VPS72 PE=1 SV=1 - [VPS72_HUMAN]
Q8N3P4	Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=1 SV=3 - [VPS8_HUMAN]
Q86WA6	Valacyclovir hydrolase OS=Homo sapiens GN=BPHL PE=1 SV=1 - [BPHL_HUMAN]

Q9ULK5	Vang-like protein 2 OS=Homo sapiens GN=VANGL2 PE=1 SV=2 - [VANG2_HUMAN]
Q6UXB2	VEGF coregulated chemokine 1 OS=Homo sapiens GN=CXCL17 PE=1 SV=1 - [VCC1_HUMAN]
Q9H8Y1	Vertnin OS=Homo sapiens GN=VRTN PE=1 SV=1 - [VRTN_HUMAN]
Q5VWC8	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 4 OS=Homo sapiens GN=HACD4 PE=1 SV=1 - [HACD4_HUMAN]
Q9NZ43	Vesicle transport protein USE1 OS=Homo sapiens GN=USE1 PE=1 SV=2 - [USE1_HUMAN]
P63027	Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=1 SV=3 - [VAMP2_HUMAN]
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 - [NSF_HUMAN]
Q9BRL7	Vesicle-trafficking protein SEC22c OS=Homo sapiens GN=SEC22C PE=1 SV=1 - [SC22C_HUMAN]
Q8NDX2	Vesicular glutamate transporter 3 OS=Homo sapiens GN=SLC17A8 PE=1 SV=1 - [VGLU3_HUMAN]
Q9HBM0	Vezatin OS=Homo sapiens GN=VEZT PE=1 SV=3 - [VEZA_HUMAN]
P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]
P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 - [VIME_HUMAN]
O60504	Vinexin OS=Homo sapiens GN=SORBS3 PE=1 SV=2 - [VINEX_HUMAN]
Q9NZR4	Visual system homeobox 1 OS=Homo sapiens GN=VSX1 PE=1 SV=2 - [VSX1_HUMAN]
Q6UXI7	Vitrin OS=Homo sapiens GN=VIT PE=2 SV=1 - [VITRN_HUMAN]
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VDAC1_HUMAN]
Q13936	Voltage-dependent L-type calcium channel subunit alpha-1C OS=Homo sapiens GN=CACNA1C PE=1 SV=4 - [CAC1C_HUMAN]
Q02641	Voltage-dependent L-type calcium channel subunit beta-1 OS=Homo sapiens GN=CACNB1 PE=2 SV=3 - [CACB1_HUMAN]
Q08289	Voltage-dependent L-type calcium channel subunit beta-2 OS=Homo sapiens GN=CACNB2 PE=1 SV=3 - [CACB2_HUMAN]
O43497	Voltage-dependent T-type calcium channel subunit alpha-1G OS=Homo sapiens GN=CACNA1G PE=2 SV=3 - [CAC1G_HUMAN]
O95180	Voltage-dependent T-type calcium channel subunit alpha-1H OS=Homo sapiens GN=CACNA1H PE=1 SV=4 - [CAC1H_HUMAN]
Q9P0X4	Voltage-dependent T-type calcium channel subunit alpha-1I OS=Homo sapiens GN=CACNA1I PE=1 SV=1 - [CAC1I_HUMAN]
Q8IWT6	Volume-regulated anion channel subunit LRRC8A OS=Homo sapiens GN=LRRC8A PE=1 SV=1 - [LRC8A_HUMAN]
Q9BXE9	Vomeronasal type-1 receptor 3 OS=Homo sapiens GN=VN1R3 PE=2 SV=1 - [VN1R3_HUMAN]
Q5TIE3	von Willebrand factor A domain-containing protein 5B1 OS=Homo sapiens GN=VWA5B1 PE=1 SV=2 - [VW5B1_HUMAN]
A3KMH1	von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2 - [VWA8_HUMAN]
Q8WY21	VPS10 domain-containing receptor SorCS1 OS=Homo sapiens GN=SORCS1 PE=1 SV=3 - [SORC1_HUMAN]
Q86VR7	V-set and immunoglobulin domain-containing protein 10-like OS=Homo sapiens GN=VSIG10L PE=2 SV=2 - [VS10L_HUMAN]
Q5VU13	V-set and immunoglobulin domain-containing protein 8 OS=Homo sapiens GN=VSIG8 PE=2 SV=1 - [VSIG8_HUMAN]
P15313	V-type proton ATPase subunit B, kidney isoform OS=Homo sapiens GN=ATP6V1B1 PE=1 SV=3 - [VATB1_HUMAN]
P21283	V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4 - [VATC1_HUMAN]
Q8N8Y2	V-type proton ATPase subunit d 2 OS=Homo sapiens GN=ATP6V0D2 PE=2 SV=1 - [VA0D2_HUMAN]
Q15904	V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2 - [VAS1_HUMAN]
Q8TF74	WAS/WASL-interacting protein family member 2 OS=Homo sapiens GN=WIPF2 PE=1 SV=1 - [WIPF2_HUMAN]
Q2M389	WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2 - [WASH7_HUMAN]
Q8IWB7	WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDFY1 PE=1 SV=1 - [WDFY1_HUMAN]
Q8IZQ1	WD repeat and FYVE domain-containing protein 3 OS=Homo sapiens GN=WDFY3 PE=1 SV=2 - [WDFY3_HUMAN]
Q6ZS81	WD repeat- and FYVE domain-containing protein 4 OS=Homo sapiens GN=WDFY4 PE=1 SV=3 - [WDFY4_HUMAN]
O75717	WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens GN=WDHD1 PE=1 SV=1 - [WDHD1_HUMAN]
Q8IZU2	WD repeat-containing protein 17 OS=Homo sapiens GN=WDR17 PE=2 SV=2 - [WDR17_HUMAN]
Q9UNX4	WD repeat-containing protein 3 OS=Homo sapiens GN=WDR3 PE=1 SV=1 - [WDR3_HUMAN]
Q8IWG1	WD repeat-containing protein 63 OS=Homo sapiens GN=WDR63 PE=2 SV=1 - [WDR63_HUMAN]
B1ANS9	WD repeat-containing protein 64 OS=Homo sapiens GN=WDR64 PE=2 SV=1 - [WDR64_HUMAN]
Q3MJ13	WD repeat-containing protein 72 OS=Homo sapiens GN=WDR72 PE=2 SV=2 - [WDR72_HUMAN]

Q5VTH9	WD repeat-containing protein 78 OS=Homo sapiens GN=WDR78 PE=2 SV=1 - [WDR78_HUMAN]
Q6ZQQ6	WD repeat-containing protein 87 OS=Homo sapiens GN=WDR87 PE=1 SV=3 - [WDR87_HUMAN]
A4D1P6	WD repeat-containing protein 91 OS=Homo sapiens GN=WDR91 PE=1 SV=2 - [WDR91_HUMAN]
Q9NXC5	WD repeat-containing protein mio OS=Homo sapiens GN=MIOS PE=1 SV=2 - [MIO_HUMAN]
P0C1S8	Wee1-like protein kinase 2 OS=Homo sapiens GN=WEE2 PE=2 SV=2 - [WEE2_HUMAN]
P30291	Wee1-like protein kinase OS=Homo sapiens GN=WEE1 PE=1 SV=2 - [WEE1_HUMAN]
Q14191	Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2 - [WRN_HUMAN]
A6NIX2	Wilms tumor protein 1-interacting protein OS=Homo sapiens GN=WTIP PE=1 SV=3 - [WTIP_HUMAN]
O95389	WNT1-inducible-signaling pathway protein 3 OS=Homo sapiens GN=WISP3 PE=1 SV=1 - [WISP3_HUMAN]
O43895	Xaa-Pro aminopeptidase 2 OS=Homo sapiens GN=XPNPEP2 PE=2 SV=3 - [XPP2_HUMAN]
Q702N8	Xin actin-binding repeat-containing protein 1 OS=Homo sapiens GN=XIRP1 PE=1 SV=1 - [XIRP1_HUMAN]
A4UGR9	Xin actin-binding repeat-containing protein 2 OS=Homo sapiens GN=XIRP2 PE=1 SV=2 - [XIRP2_HUMAN]
Q5GH72	XK-related protein 7 OS=Homo sapiens GN=XKR7 PE=2 SV=1 - [XKR7_HUMAN]
Q9H6D3	XK-related protein 8 OS=Homo sapiens GN=XKR8 PE=1 SV=1 - [XKR8_HUMAN]
Q6P2D8	X-ray radiation resistance-associated protein 1 OS=Homo sapiens GN=XRRA1 PE=2 SV=2 - [XRRA1_HUMAN]
Q9H1B5	Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2 - [XYLT2_HUMAN]
Q9Y5A9	YTH domain-containing family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2 - [YTHD2_HUMAN]
Q96MU7	YTH domain-containing protein 1 OS=Homo sapiens GN=YTHDC1 PE=1 SV=3 - [YTDC1_HUMAN]
Q8IY57	YY1-associated factor 2 OS=Homo sapiens GN=YAF2 PE=1 SV=3 - [YAF2_HUMAN]
Q9H869	YY1-associated protein 1 OS=Homo sapiens GN=YY1AP1 PE=1 SV=2 - [YYAP1_HUMAN]
Q99592	Zinc finger and BTB domain-containing protein 18 OS=Homo sapiens GN=ZBTB18 PE=1 SV=1 - [ZBT18_HUMAN]
Q9ULJ3	Zinc finger and BTB domain-containing protein 21 OS=Homo sapiens GN=ZBTB21 PE=1 SV=2 - [ZBT21_HUMAN]
Q8NCN2	Zinc finger and BTB domain-containing protein 34 OS=Homo sapiens GN=ZBTB34 PE=2 SV=4 - [ZBT34_HUMAN]
Q5SVQ8	Zinc finger and BTB domain-containing protein 41 OS=Homo sapiens GN=ZBTB41 PE=1 SV=1 - [ZBT41_HUMAN]
Q15916	Zinc finger and BTB domain-containing protein 6 OS=Homo sapiens GN=ZBTB6 PE=1 SV=1 - [ZBTB6_HUMAN]
O15156	Zinc finger and BTB domain-containing protein 7B OS=Homo sapiens GN=ZBTB7B PE=1 SV=2 - [ZBT7B_HUMAN]
Q96SZ4	Zinc finger and SCAN domain-containing protein 10 OS=Homo sapiens GN=ZSCAN10 PE=1 SV=1 - [ZSC10_HUMAN]
Q96IU2	Zinc finger BED domain-containing protein 3 OS=Homo sapiens GN=ZBED3 PE=1 SV=1 - [ZBED3_HUMAN]
O75132	Zinc finger BED domain-containing protein 4 OS=Homo sapiens GN=ZBED4 PE=1 SV=2 - [ZBED4_HUMAN]
Q49AG3	Zinc finger BED domain-containing protein 5 OS=Homo sapiens GN=ZBED5 PE=2 SV=2 - [ZBED5_HUMAN]
P86452	Zinc finger BED domain-containing protein 6 OS=Homo sapiens GN=ZBED6 PE=3 SV=1 - [ZBED6_HUMAN]
O75152	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3 - [ZC11A_HUMAN]
Q5T200	Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1 - [ZC3HD_HUMAN]
Q86VM9	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=1 SV=2 - [ZCH18_HUMAN]
Q9C0B9	Zinc finger CCHC domain-containing protein 2 OS=Homo sapiens GN=ZCCHC2 PE=1 SV=6 - [ZCHC2_HUMAN]
Q9NUD5	Zinc finger CCHC domain-containing protein 3 OS=Homo sapiens GN=ZCCHC3 PE=1 SV=1 - [ZCHC3_HUMAN]
Q9H5U6	Zinc finger CCHC domain-containing protein 4 OS=Homo sapiens GN=ZCCHC4 PE=1 SV=3 - [ZCHC4_HUMAN]
P37275	Zinc finger E-box-binding homeobox 1 OS=Homo sapiens GN=ZEB1 PE=1 SV=2 - [ZEB1_HUMAN]
O60315	Zinc finger E-box-binding homeobox 2 OS=Homo sapiens GN=ZEB2 PE=1 SV=1 - [ZEB2_HUMAN]
Q68DK2	Zinc finger FYVE domain-containing protein 26 OS=Homo sapiens GN=ZFYVE26 PE=1 SV=3 - [ZFY26_HUMAN]
O95405	Zinc finger FYVE domain-containing protein 9 OS=Homo sapiens GN=ZFYVE9 PE=1 SV=2 - [ZFYV9_HUMAN]
Q9C0A1	Zinc finger homeobox protein 2 OS=Homo sapiens GN=ZFHX2 PE=2 SV=3 - [ZFHX2_HUMAN]
Q86UP3	Zinc finger homeobox protein 4 OS=Homo sapiens GN=ZFHX4 PE=1 SV=1 - [ZFHX4_HUMAN]
O95789	Zinc finger MYM-type protein 6 OS=Homo sapiens GN=ZMYM6 PE=2 SV=2 - [ZMYM6_HUMAN]
Q8IZC7	Zinc finger protein 101 OS=Homo sapiens GN=ZNF101 PE=1 SV=1 - [ZN101_HUMAN]
Q9H2Y7	Zinc finger protein 106 OS=Homo sapiens GN=ZNF106 PE=1 SV=1 - [ZN106_HUMAN]

P52737	Zinc finger protein 136 OS=Homo sapiens GN=ZNF136 PE=1 SV=1 - [ZN136_HUMAN]
P52746	Zinc finger protein 142 OS=Homo sapiens GN=ZNF142 PE=2 SV=4 - [ZN142_HUMAN]
Q13106	Zinc finger protein 154 OS=Homo sapiens GN=ZNF154 PE=2 SV=3 - [ZN154_HUMAN]
P17020	Zinc finger protein 16 OS=Homo sapiens GN=ZNF16 PE=1 SV=3 - [ZNF16_HUMAN]
P98182	Zinc finger protein 200 OS=Homo sapiens GN=ZNF200 PE=2 SV=2 - [ZN200_HUMAN]
O43345	Zinc finger protein 208 OS=Homo sapiens GN=ZNF208 PE=2 SV=2 - [ZN208_HUMAN]
Q9UDV6	Zinc finger protein 212 OS=Homo sapiens GN=ZNF212 PE=1 SV=3 - [ZN212_HUMAN]
Q9UNY5	Zinc finger protein 232 OS=Homo sapiens GN=ZNF232 PE=1 SV=1 - [ZN232_HUMAN]
P17035	Zinc finger protein 28 OS=Homo sapiens GN=ZNF28 PE=2 SV=5 - [ZNF28_HUMAN]
Q9HBT8	Zinc finger protein 286A OS=Homo sapiens GN=ZNF286A PE=1 SV=1 - [Z286A_HUMAN]
Q96JL9	Zinc finger protein 333 OS=Homo sapiens GN=ZNF333 PE=2 SV=3 - [ZN333_HUMAN]
Q9Y3M9	Zinc finger protein 337 OS=Homo sapiens GN=ZNF337 PE=1 SV=2 - [ZN337_HUMAN]
Q06730	Zinc finger protein 33A OS=Homo sapiens GN=ZNF33A PE=1 SV=3 - [ZN33A_HUMAN]
Q9BYN7	Zinc finger protein 341 OS=Homo sapiens GN=ZNF341 PE=1 SV=2 - [ZN341_HUMAN]
Q96SE7	Zinc finger protein 347 OS=Homo sapiens GN=ZNF347 PE=1 SV=2 - [ZN347_HUMAN]
Q9Y6Q3	Zinc finger protein 37 homolog OS=Homo sapiens GN=ZFP37 PE=2 SV=3 - [ZFP37_HUMAN]
P17032	Zinc finger protein 37A OS=Homo sapiens GN=ZNF37A PE=2 SV=3 - [ZN37A_HUMAN]
Q96PM9	Zinc finger protein 385A OS=Homo sapiens GN=ZNF385A PE=1 SV=2 - [Z385A_HUMAN]
Q53GI3	Zinc finger protein 394 OS=Homo sapiens GN=ZNF394 PE=1 SV=2 - [ZN394_HUMAN]
P15822	Zinc finger protein 40 OS=Homo sapiens GN=HIVEP1 PE=1 SV=3 - [ZEP1_HUMAN]
Q8TAU3	Zinc finger protein 417 OS=Homo sapiens GN=ZNF417 PE=1 SV=2 - [ZN417_HUMAN]
Q96MM3	Zinc finger protein 42 homolog OS=Homo sapiens GN=ZFP42 PE=1 SV=2 - [ZFP42_HUMAN]
Q9BUY5	Zinc finger protein 426 OS=Homo sapiens GN=ZNF426 PE=1 SV=1 - [ZN426_HUMAN]
Q9H8G1	Zinc finger protein 430 OS=Homo sapiens GN=ZNF430 PE=1 SV=3 - [ZN430_HUMAN]
Q7Z4V0	Zinc finger protein 438 OS=Homo sapiens GN=ZNF438 PE=2 SV=1 - [ZN438_HUMAN]
Q9Y4E5	Zinc finger protein 451 OS=Homo sapiens GN=ZNF451 PE=1 SV=2 - [ZN451_HUMAN]
Q8TF39	Zinc finger protein 483 OS=Homo sapiens GN=ZNF483 PE=1 SV=3 - [ZN483_HUMAN]
Q9P255	Zinc finger protein 492 OS=Homo sapiens GN=ZNF492 PE=2 SV=2 - [ZN492_HUMAN]
Q96IT1	Zinc finger protein 496 OS=Homo sapiens GN=ZNF496 PE=1 SV=1 - [ZN496_HUMAN]
Q96KM6	Zinc finger protein 512B OS=Homo sapiens GN=ZNF512B PE=1 SV=1 - [Z512B_HUMAN]
Q6AHZ1	Zinc finger protein 518A OS=Homo sapiens GN=ZNF518A PE=2 SV=2 - [Z518A_HUMAN]
Q8NB42	Zinc finger protein 527 OS=Homo sapiens GN=ZNF527 PE=2 SV=2 - [ZN527_HUMAN]
O15090	Zinc finger protein 536 OS=Homo sapiens GN=ZNF536 PE=1 SV=3 - [ZN536_HUMAN]
Q9H0D2	Zinc finger protein 541 OS=Homo sapiens GN=ZNF541 PE=2 SV=3 - [ZN541_HUMAN]
Q8N184	Zinc finger protein 567 OS=Homo sapiens GN=ZNF567 PE=1 SV=3 - [ZN567_HUMAN]
Q96N58	Zinc finger protein 578 OS=Homo sapiens GN=ZNF578 PE=2 SV=2 - [ZN578_HUMAN]
Q92610	Zinc finger protein 592 OS=Homo sapiens GN=ZNF592 PE=1 SV=2 - [ZN592_HUMAN]
O15014	Zinc finger protein 609 OS=Homo sapiens GN=ZNF609 PE=1 SV=2 - [ZN609_HUMAN]
Q6AZW8	Zinc finger protein 660 OS=Homo sapiens GN=ZNF660 PE=1 SV=1 - [ZN660_HUMAN]
Q96CS4	Zinc finger protein 689 OS=Homo sapiens GN=ZNF689 PE=2 SV=1 - [ZN689_HUMAN]
Q9H0M5	Zinc finger protein 700 OS=Homo sapiens GN=ZNF700 PE=2 SV=1 - [ZN700_HUMAN]
Q6ZNC4	Zinc finger protein 704 OS=Homo sapiens GN=ZNF704 PE=1 SV=1 - [ZN704_HUMAN]
A8MVS1	Zinc finger protein 705F OS=Homo sapiens GN=ZNF705F PE=3 SV=1 - [Z705F_HUMAN]
P0DKX0	Zinc finger protein 728 OS=Homo sapiens GN=ZNF728 PE=3 SV=1 - [ZN728_HUMAN]
Q96N20	Zinc finger protein 75A OS=Homo sapiens GN=ZNF75A PE=2 SV=1 - [ZN75A_HUMAN]
Q6ZMW2	Zinc finger protein 782 OS=Homo sapiens GN=ZNF782 PE=2 SV=1 - [ZN782_HUMAN]
Q3KP31	Zinc finger protein 791 OS=Homo sapiens GN=ZNF791 PE=2 SV=1 - [ZN791_HUMAN]
Q7Z570	Zinc finger protein 804A OS=Homo sapiens GN=ZNF804A PE=1 SV=3 - [Z804A_HUMAN]
P0C7X5	Zinc finger protein 806 OS=Homo sapiens GN=ZNF806 PE=3 SV=1 - [ZN806_HUMAN]
Q0VGE8	Zinc finger protein 816 OS=Homo sapiens GN=ZNF816 PE=2 SV=2 - [ZN816_HUMAN]
Q8N141	Zinc finger protein 82 homolog OS=Homo sapiens GN=ZFP82 PE=2 SV=1 - [ZFP82_HUMAN]
O75541	Zinc finger protein 821 OS=Homo sapiens GN=ZNF821 PE=1 SV=3 - [ZN821_HUMAN]

Q5JPB2	Zinc finger protein 831 OS=Homo sapiens GN=ZNF831 PE=2 SV=4 - [ZN831_HUMAN]
A6NHJ4	Zinc finger protein 860 OS=Homo sapiens GN=ZNF860 PE=2 SV=3 - [ZN860_HUMAN]
O60290	Zinc finger protein 862 OS=Homo sapiens GN=ZNF862 PE=2 SV=2 - [ZN862_HUMAN]
A8MXY4	Zinc finger protein 99 OS=Homo sapiens GN=ZNF99 PE=2 SV=3 - [ZNF99_HUMAN]
Q6ZN18	Zinc finger protein AEBP2 OS=Homo sapiens GN=AEBP2 PE=1 SV=2 - [AEBP2_HUMAN]
Q92782	Zinc finger protein neuro-d4 OS=Homo sapiens GN=DPF1 PE=2 SV=2 - [DPF1_HUMAN]
Q63HK3	Zinc finger protein with KRAB and SCAN domains 2 OS=Homo sapiens GN=ZKSCAN2 PE=1 SV=2 - [ZKSC2_HUMAN]
O95218	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2 - [ZRAB2_HUMAN]
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6 - [ZZEF1_HUMAN]
Q9Y6X8	Zinc fingers and homeoboxes protein 2 OS=Homo sapiens GN=ZHX2 PE=1 SV=1 - [ZHX2_HUMAN]
Q9BQ52	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2 - [RNZ2_HUMAN]
Q9BRY0	Zinc transporter ZIP3 OS=Homo sapiens GN=SLC39A3 PE=1 SV=2 - [S39A3_HUMAN]
Q9NUM3	Zinc transporter ZIP9 OS=Homo sapiens GN=SLC39A9 PE=2 SV=2 - [S39A9_HUMAN]
Q401N2	Zinc-activated ligand-gated ion channel OS=Homo sapiens GN=ZACN PE=1 SV=2 - [ZACN_HUMAN]
Q15942	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1 - [ZYX_HUMAN]

Appendix C

Table VII. Identified membrane glycoproteins from Tn-negative, blood group A negative, STn-positive basal-like chemoresistant tumors, with O-GalNAc as posttranslational modifications after neuraminiase treatment.

Accession	Description
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]
P51178	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Homo sapiens GN=PLCD1 PE=1 SV=2 - [PLCD1_HUMAN]
Q8N3E9	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3 OS=Homo sapiens GN=PLCD3 PE=1 SV=3 - [PLCD3_HUMAN]
Q9P212	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 OS=Homo sapiens GN=PLCE1 PE=1 SV=3 - [PLCE1_HUMAN]
Q4KWH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens GN=PLCH1 PE=1 SV=1 - [PLCH1_HUMAN]
O75038	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 OS=Homo sapiens GN=PLCH2 PE=2 SV=3 - [PLCH2_HUMAN]
P19174	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1 PE=1 SV=1 - [PLCG1_HUMAN]
P16885	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 OS=Homo sapiens GN=PLCG2 PE=1 SV=4 - [PLCG2_HUMAN]
P34969	5-hydroxytryptamine receptor 7 OS=Homo sapiens GN=HTR7 PE=1 SV=2 - [5HT7R_HUMAN]
Q96FT7	Acid-sensing ion channel 4 OS=Homo sapiens GN=ASIC4 PE=1 SV=2 - [ASIC4_HUMAN]
Q8NER5	Activin receptor type-1C OS=Homo sapiens GN=ACVR1C PE=1 SV=1 - [ACV1C_HUMAN]
O95996	Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1 - [APC2_HUMAN]
P25054	Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2 - [APC_HUMAN]
P51828	Adenylate cyclase type 7 OS=Homo sapiens GN=ADCY7 PE=2 SV=1 - [ADCY7_HUMAN]
O60503	Adenylate cyclase type 9 OS=Homo sapiens GN=ADCY9 PE=1 SV=4 - [ADCY9_HUMAN]
O60241	Adhesion G protein-coupled receptor B2 OS=Homo sapiens GN=ADGRB2 PE=1 SV=2 - [AGRB2_HUMAN]
Q9UHX3	Adhesion G protein-coupled receptor E2 OS=Homo sapiens GN=ADGRE2 PE=1 SV=2 - [AGRE2_HUMAN]
Q10588	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2 OS=Homo sapiens GN=BST1 PE=1 SV=2 - [BST1_HUMAN]
P55196	Afadin OS=Homo sapiens GN=MLLT4 PE=1 SV=3 - [AFAD_HUMAN]
P55008	Allograft inflammatory factor 1 OS=Homo sapiens GN=AIF1 PE=1 SV=1 - [AIF1_HUMAN]
P30533	Alpha-2-macroglobulin receptor-associated protein OS=Homo sapiens GN=LRPAP1 PE=1 SV=1 - [AMRP_HUMAN]
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]
P35611	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2 - [ADDA_HUMAN]
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]
Q969X2	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 OS=Homo sapiens GN=ST6GALNAC6 PE=1 SV=1 - [SIA7F_HUMAN]
P51172	Amiloride-sensitive sodium channel subunit delta OS=Homo sapiens GN=SCNN1D PE=1 SV=2 - [SCNND_HUMAN]
Q99767	Amyloid beta A4 precursor protein-binding family A member 2 OS=Homo sapiens GN=APBA2 PE=1 SV=3 - [APBA2_HUMAN]
Q8IY63	Angiomotin-like protein 1 OS=Homo sapiens GN=AMOTL1 PE=1 SV=1 - [AMOL1_HUMAN]
P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]
P09525	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4 - [ANXA4_HUMAN]
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]
P20073	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 - [ANXA7_HUMAN]
Q9NQ90	Anoctamin-2 OS=Homo sapiens GN=ANO2 PE=1 SV=2 - [ANO2_HUMAN]
Q9HCE9	Anoctamin-8 OS=Homo sapiens GN=ANO8 PE=1 SV=3 - [ANO8_HUMAN]

Q8N7J2	APC membrane recruitment protein 2 OS=Homo sapiens GN=AMER2 PE=1 SV=3 - [AMER2_HUMAN]
Q8N944	APC membrane recruitment protein 3 OS=Homo sapiens GN=AMER3 PE=1 SV=2 - [AMER3_HUMAN]
Q96P48	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3 - [ARAP1_HUMAN]
Q8WWN8	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=ARAP3 PE=1 SV=1 - [ARAP3_HUMAN]
Q8N5I2	Arrestin domain-containing protein 1 OS=Homo sapiens GN=ARRDC1 PE=1 SV=1 - [ARRD1_HUMAN]
Q8TBH0	Arrestin domain-containing protein 2 OS=Homo sapiens GN=ARRDC2 PE=2 SV=2 - [ARRD2_HUMAN]
P15848	Arylsulfatase B OS=Homo sapiens GN=ARSB PE=1 SV=1 - [ARSB_HUMAN]
O14525	Astrotactin-1 OS=Homo sapiens GN=ASTN1 PE=2 SV=3 - [ASTN1_HUMAN]
Q9Y2T1	Axin-2 OS=Homo sapiens GN=AXIN2 PE=1 SV=1 - [AXIN2_HUMAN]
Q9HCM4	Band 4.1-like protein 5 OS=Homo sapiens GN=EPB41L5 PE=1 SV=3 - [E41L5_HUMAN]
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 - [PGBM_HUMAN]
Q8WV28	B-cell linker protein OS=Homo sapiens GN=BLNK PE=1 SV=2 - [BLNK_HUMAN]
Q5H9F3	BCL-6 corepressor-like protein 1 OS=Homo sapiens GN=BCORL1 PE=1 SV=1 - [BCORL_HUMAN]
Q8N1M1	Bestrophin-3 OS=Homo sapiens GN=BEST3 PE=2 SV=1 - [BEST3_HUMAN]
Q13884	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3 - [SNTB1_HUMAN]
Q7Z7B7	Beta-defensin 132 OS=Homo sapiens GN=DEFB132 PE=3 SV=1 - [DB132_HUMAN]
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]
P32247	Bombesin receptor subtype-3 OS=Homo sapiens GN=BRS3 PE=1 SV=1 - [BRS3_HUMAN]
P80723	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2 - [BASP1_HUMAN]
P38398	Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2 - [BRCA1_HUMAN]
Q8NCU7	C2 calcium-dependent domain-containing protein 4A OS=Homo sapiens GN=C2CD4A PE=2 SV=2 - [C2C4A_HUMAN]
A6NLJ0	C2 calcium-dependent domain-containing protein 4B OS=Homo sapiens GN=C2CD4B PE=2 SV=1 - [C2C4B_HUMAN]
Q8TF44	C2 calcium-dependent domain-containing protein 4C OS=Homo sapiens GN=C2CD4C PE=1 SV=2 - [C2C4C_HUMAN]
Q8IZJ3	C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens GN=CPAMD8 PE=1 SV=2 - [CPMD8_HUMAN]
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]
P55287	Cadherin-11 OS=Homo sapiens GN=CDH11 PE=2 SV=2 - [CAD11_HUMAN]
Q9H251	Cadherin-23 OS=Homo sapiens GN=CDH23 PE=1 SV=2 - [CAD23_HUMAN]
Q8IXH8	Cadherin-like protein 26 OS=Homo sapiens GN=CDH26 PE=2 SV=3 - [CAD26_HUMAN]
P30988	Calcitonin receptor OS=Homo sapiens GN=CALCR PE=1 SV=2 - [CALCR_HUMAN]
Q96NX5	Calcium/calmodulin-dependent protein kinase type 1G OS=Homo sapiens GN=CAMK1G PE=1 SV=3 - [KCC1G_HUMAN]
Q9UQM7	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Homo sapiens GN=CAMK2A PE=1 SV=2 - [KCC2A_HUMAN]
Q12791	Calcium-activated potassium channel subunit alpha-1 OS=Homo sapiens GN=KCNMA1 PE=1 SV=2 - [KCMA1_HUMAN]
Q86UW7	Calcium-dependent secretion activator 2 OS=Homo sapiens GN=CADPS2 PE=1 SV=2 - [CAPS2_HUMAN]
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [CAN1_HUMAN]
Q9HC96	Calpain-10 OS=Homo sapiens GN=CAPN10 PE=1 SV=2 - [CAN10_HUMAN]
P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]
Q9BXL7	Caspase recruitment domain-containing protein 11 OS=Homo sapiens GN=CARD11 PE=1 SV=3 - [CAR11_HUMAN]
Q9BXL6	Caspase recruitment domain-containing protein 14 OS=Homo sapiens GN=CARD14 PE=1 SV=2 - [CAR14_HUMAN]
Q92851	Caspase-10 OS=Homo sapiens GN=CASP10 PE=1 SV=3 - [CASPA_HUMAN]
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 - [CATA_HUMAN]
P26232	Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5 - [CTNA2_HUMAN]
P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]
P52569	Cationic amino acid transporter 2 OS=Homo sapiens GN=SLC7A2 PE=1 SV=2 - [CTR2_HUMAN]
P46092	C-C chemokine receptor type 10 OS=Homo sapiens GN=CCR10 PE=1 SV=3 - [CCR10_HUMAN]
P51684	C-C chemokine receptor type 6 OS=Homo sapiens GN=CCR6 PE=2 SV=2 - [CCR6_HUMAN]
Q6YHK3	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2 - [CD109_HUMAN]
O95971	CD160 antigen OS=Homo sapiens GN=CD160 PE=1 SV=1 - [BY55_HUMAN]

Q9Y5K6	CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 - [CD2AP_HUMAN]
P16070	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3 - [CD44_HUMAN]
Q99795	Cell surface A33 antigen OS=Homo sapiens GN=GPA33 PE=1 SV=1 - [GPA33_HUMAN]
P35523	Chloride channel protein 1 OS=Homo sapiens GN=CLCN1 PE=1 SV=3 - [CLCN1_HUMAN]
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]
P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 - [CLCB_HUMAN]
Q6UXG3	CMRF35-like molecule 9 OS=Homo sapiens GN=CD300LG PE=1 SV=2 - [CLM9_HUMAN]
P12259	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4 - [FA5_HUMAN]
P00451	Coagulation factor VIII OS=Homo sapiens GN=F8 PE=1 SV=1 - [FA8_HUMAN]
P00748	Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3 - [FA12_HUMAN]
Q8IWY9	Codanin-1 OS=Homo sapiens GN=CDAN1 PE=1 SV=4 - [CDAN1_HUMAN]
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]
Q5KU26	Collectin-12 OS=Homo sapiens GN=COLEC12 PE=1 SV=3 - [COL12_HUMAN]
P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HUMAN]
P01031	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4 - [CO5_HUMAN]
Q9NPY3	Complement component C1q receptor OS=Homo sapiens GN=CD93 PE=1 SV=3 - [C1QR1_HUMAN]
P10643	Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2 - [CO7_HUMAN]
P17927	Complement receptor type 1 OS=Homo sapiens GN=CR1 PE=1 SV=3 - [CR1_HUMAN]
O94779	Contactin-5 OS=Homo sapiens GN=CNTN5 PE=1 SV=2 - [CNTN5_HUMAN]
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]
Q04656	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3 - [ATP7A_HUMAN]
P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]
Q9BR76	Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 - [COR1B_HUMAN]
P49238	CX3C chemokine receptor 1 OS=Homo sapiens GN=CX3CR1 PE=1 SV=1 - [CX3C1_HUMAN]
P61073	C-X-C chemokine receptor type 4 OS=Homo sapiens GN=CXCR4 PE=1 SV=1 - [CXCR4_HUMAN]
P13569	Cystic fibrosis transmembrane conductance regulator OS=Homo sapiens GN=CFTR PE=1 SV=3 - [CFTR_HUMAN]
Q9UPY5	Cystine/glutamate transporter OS=Homo sapiens GN=SLC7A11 PE=1 SV=1 - [XCT_HUMAN]
O95727	Cytotoxic and regulatory T-cell molecule OS=Homo sapiens GN=CRTAM PE=1 SV=2 - [CRTAM_HUMAN]
P53355	Death-associated protein kinase 1 OS=Homo sapiens GN=DAPK1 PE=1 SV=6 - [DAPK1_HUMAN]
A4D2P6	Delphilin OS=Homo sapiens GN=GRID2IP PE=3 SV=2 - [GRD2I_HUMAN]
P17661	Desmin OS=Homo sapiens GN=DES PE=1 SV=3 - [DESM_HUMAN]
Q14574	Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3 - [DSC3_HUMAN]
Q9Y6T7	Diacylglycerol kinase beta OS=Homo sapiens GN=DGKB PE=2 SV=2 - [DGKB_HUMAN]
Q16760	Diacylglycerol kinase delta OS=Homo sapiens GN=DGKD PE=1 SV=4 - [DGKD_HUMAN]
Q5KSL6	Diacylglycerol kinase kappa OS=Homo sapiens GN=DGKK PE=1 SV=1 - [DGKK_HUMAN]
O94907	Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1 - [DKK1_HUMAN]
Q8TF46	DIS3-like exonuclease 1 OS=Homo sapiens GN=DIS3L PE=1 SV=2 - [DI3L1_HUMAN]
P98082	Disabled homolog 2 OS=Homo sapiens GN=DAB2 PE=1 SV=3 - [DAB2_HUMAN]
Q9Y4D1	Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2 - [DAAM1_HUMAN]
O14672	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1 - [ADA10_HUMAN]
P78536	Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1 - [ADA17_HUMAN]
Q9UKJ8	Disintegrin and metalloproteinase domain-containing protein 21 OS=Homo sapiens GN=ADAM21 PE=2 SV=2 - [ADA21_HUMAN]
Q92796	Disks large homolog 3 OS=Homo sapiens GN=DLG3 PE=1 SV=2 - [DLG3_HUMAN]
O14490	Disks large-associated protein 1 OS=Homo sapiens GN=DLGAP1 PE=1 SV=1 - [DLGP1_HUMAN]
Q9P1A6	Disks large-associated protein 2 OS=Homo sapiens GN=DLGAP2 PE=1 SV=4 - [DLGP2_HUMAN]
O95886	Disks large-associated protein 3 OS=Homo sapiens GN=DLGAP3 PE=1 SV=3 - [DLGP3_HUMAN]
O60469	Down syndrome cell adhesion molecule OS=Homo sapiens GN=DSCAM PE=1 SV=2 - [DSCAM_HUMAN]
Q8TD84	Down syndrome cell adhesion molecule-like protein 1 OS=Homo sapiens GN=DSCAML1 PE=1 SV=2 - [DSCL1_HUMAN]
Q8N1N2	Dynactin-associated protein OS=Homo sapiens GN=DYNAP PE=1 SV=1 - [DYNAP_HUMAN]
Q05193	Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 SV=2 - [DYN1_HUMAN]

Q96M86	Dynein heavy chain domain-containing protein 1 OS=Homo sapiens GN=DNHD1 PE=2 SV=2 - [DNHD1_HUMAN]
Q9GZS0	Dynein intermediate chain 2, axonemal OS=Homo sapiens GN=DNAI2 PE=1 SV=2 - [DNAI2_HUMAN]
O75923	Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1 - [DYSF_HUMAN]
Q03001	Dystonin OS=Homo sapiens GN=DST PE=1 SV=4 - [DYST_HUMAN]
P11532	Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3 - [DMD_HUMAN]
A2CJ06	Dystrotelin OS=Homo sapiens GN=DYTN PE=2 SV=1 - [DYTN_HUMAN]
Q15075	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]
Q14244	Ensconsin OS=Homo sapiens GN=MAP7 PE=1 SV=1 - [MAP7_HUMAN]
P29320	Ephrin type-A receptor 3 OS=Homo sapiens GN=EPHA3 PE=1 SV=2 - [EPHA3_HUMAN]
Q15375	Ephrin type-A receptor 7 OS=Homo sapiens GN=EPHA7 PE=1 SV=3 - [EPHA7_HUMAN]
P29323	Ephrin type-B receptor 2 OS=Homo sapiens GN=EPHB2 PE=1 SV=5 - [EPHB2_HUMAN]
P98172	Ephrin-B1 OS=Homo sapiens GN=EFNB1 PE=1 SV=1 - [EFNB1_HUMAN]
Q9UBC2	Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens GN=EPS15L1 PE=1 SV=1 - [EP15R_HUMAN]
P16452	Erythrocyte membrane protein band 4.2 OS=Homo sapiens GN=EPB42 PE=1 SV=3 - [EPB42_HUMAN]
Q8IWU5	Extracellular sulfatase Sulf-2 OS=Homo sapiens GN=SULF2 PE=1 SV=1 - [SULF2_HUMAN]
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]
P08F94	Fibrocystin OS=Homo sapiens GN=PKHD1 PE=1 SV=1 - [PKHD1_HUMAN]
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]
Q9P278	Folliculin-interacting protein 2 OS=Homo sapiens GN=FNIP2 PE=1 SV=2 - [FNIP2_HUMAN]
Q68DA7	Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=3 - [FMN1_HUMAN]
Q8IVF7	Formin-like protein 3 OS=Homo sapiens GN=FMNL3 PE=1 SV=3 - [FMNL3_HUMAN]
Q7Z2K8	G protein-regulated inducer of neurite outgrowth 1 OS=Homo sapiens GN=GPRIN1 PE=2 SV=2 - [GRIN1_HUMAN]
P48169	Gamma-aminobutyric acid receptor subunit alpha-4 OS=Homo sapiens GN=GABRA4 PE=2 SV=2 - [GBRA4_HUMAN]
Q99928	Gamma-aminobutyric acid receptor subunit gamma-3 OS=Homo sapiens GN=GABRG3 PE=2 SV=2 - [GBRG3_HUMAN]
Q9UJ14	Gamma-glutamyltransferase 7 OS=Homo sapiens GN=GGT7 PE=1 SV=2 - [GGT7_HUMAN]
Q9BX51	Gamma-glutamyltransferase light chain 1 OS=Homo sapiens GN=GGTLC1 PE=2 SV=2 - [GGTL1_HUMAN]
Q969M2	Gap junction alpha-10 protein OS=Homo sapiens GN=GJA10 PE=2 SV=1 - [CXA10_HUMAN]
O95452	Gap junction beta-6 protein OS=Homo sapiens GN=GJB6 PE=1 SV=2 - [CXB6_HUMAN]
Q3V6T2	Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2 - [GRDN_HUMAN]
P48058	Glutamate receptor 4 OS=Homo sapiens GN=GRIA4 PE=2 SV=2 - [GRIA4_HUMAN]
Q12879	Glutamate receptor ionotropic, NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1 - [NMDE1_HUMAN]
Q9Y3R0	Glutamate receptor-interacting protein 1 OS=Homo sapiens GN=GRIP1 PE=1 SV=3 - [GRIP1_HUMAN]
Q9C0E4	Glutamate receptor-interacting protein 2 OS=Homo sapiens GN=GRIP2 PE=1 SV=3 - [GRIP2_HUMAN]
O75311	Glycine receptor subunit alpha-3 OS=Homo sapiens GN=GLRA3 PE=2 SV=2 - [GLRA3_HUMAN]
P46091	G-protein coupled receptor 1 OS=Homo sapiens GN=GPR1 PE=1 SV=2 - [GPR1_HUMAN]
Q96PE1	G-protein coupled receptor 124 OS=Homo sapiens GN=GPR124 PE=1 SV=2 - [GP124_HUMAN]
Q8WXG9	G-protein coupled receptor 98 OS=Homo sapiens GN=GPR98 PE=1 SV=2 - [GPR98_HUMAN]
Q9UQC2	GRB2-associated-binding protein 2 OS=Homo sapiens GN=GAB2 PE=1 SV=1 - [GAB2_HUMAN]
O95661	GTP-binding protein Di-Ras3 OS=Homo sapiens GN=DIRAS3 PE=1 SV=1 - [DIRA3_HUMAN]
P55042	GTP-binding protein RAD OS=Homo sapiens GN=RRAD PE=1 SV=2 - [RAD_HUMAN]
Q96QV1	Hedgehog-interacting protein OS=Homo sapiens GN=HHIP PE=1 SV=3 - [HHIP_HUMAN]
P08581	Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4 - [MET_HUMAN]
Q8WWV6	High affinity immunoglobulin alpha and immunoglobulin mu Fc receptor OS=Homo sapiens GN=FCAMR PE=1 SV=1 - [FCAMR_HUMAN]
Q9H3N8	Histamine H4 receptor OS=Homo sapiens GN=HRH4 PE=1 SV=2 - [HRH4_HUMAN]
P16188	HLA class I histocompatibility antigen, A-30 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2 - [1A30_HUMAN]
P30459	HLA class I histocompatibility antigen, A-74 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 - [1A74_HUMAN]
P01889	HLA class I histocompatibility antigen, B-7 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=3 - [1B07_HUMAN]

P30504	HLA class I histocompatibility antigen, Cw-4 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1 - [1C04_HUMAN]
P01909	HLA class II histocompatibility antigen, DQ alpha 1 chain OS=Homo sapiens GN=HLA-DQA1 PE=1 SV=1 - [DQA1_HUMAN]
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]
Q92819	Hyaluronan synthase 2 OS=Homo sapiens GN=HAS2 PE=2 SV=1 - [HYAS2_HUMAN]
Q5DX21	Immunoglobulin superfamily member 11 OS=Homo sapiens GN=IGSF11 PE=2 SV=3 - [IGS11_HUMAN]
Q93033	Immunoglobulin superfamily member 2 OS=Homo sapiens GN=CD101 PE=1 SV=2 - [IGSF2_HUMAN]
Q9NSI5	Immunoglobulin superfamily member 5 OS=Homo sapiens GN=IGSF5 PE=2 SV=2 - [IGSF5_HUMAN]
Q969P0	Immunoglobulin superfamily member 8 OS=Homo sapiens GN=IGSF8 PE=1 SV=1 - [IGSF8_HUMAN]
Q86SU0	Immunoglobulin-like domain-containing receptor 1 OS=Homo sapiens GN=ILDR1 PE=1 SV=2 - [ILDR1_HUMAN]
Q9H160	Inhibitor of growth protein 2 OS=Homo sapiens GN=ING2 PE=1 SV=2 - [ING2_HUMAN]
P06213	Insulin receptor OS=Homo sapiens GN=INSR PE=1 SV=4 - [INSR_HUMAN]
P35568	Insulin receptor substrate 1 OS=Homo sapiens GN=IRS1 PE=1 SV=1 - [IRS1_HUMAN]
Q9Y4H2	Insulin receptor substrate 2 OS=Homo sapiens GN=IRS2 PE=1 SV=2 - [IRS2_HUMAN]
P08069	Insulin-like growth factor 1 receptor OS=Homo sapiens GN=IGF1R PE=1 SV=1 - [IGF1R_HUMAN]
Q9NQX7	Integral membrane protein 2C OS=Homo sapiens GN=ITM2C PE=1 SV=1 - [ITM2C_HUMAN]
P23229	Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5 - [ITA6_HUMAN]
Q13683	Integrin alpha-7 OS=Homo sapiens GN=ITGA7 PE=1 SV=3 - [ITA7_HUMAN]
Q13349	Integrin alpha-D OS=Homo sapiens GN=ITGAD PE=1 SV=2 - [ITAD_HUMAN]
P06756	Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2 - [ITAV_HUMAN]
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]
P05106	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2 - [ITB3_HUMAN]
P16144	Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5 - [ITB4_HUMAN]
P26012	Integrin beta-8 OS=Homo sapiens GN=ITGB8 PE=2 SV=1 - [ITB8_HUMAN]
P01579	Interferon gamma OS=Homo sapiens GN=IFNG PE=1 SV=1 - [IFNG_HUMAN]
Q16552	Interleukin-17A OS=Homo sapiens GN=IL17A PE=1 SV=1 - [IL17_HUMAN]
Q13478	Interleukin-18 receptor 1 OS=Homo sapiens GN=IL18R1 PE=1 SV=1 - [IL18R_HUMAN]
O15554	Intermediate conductance calcium-activated potassium channel protein 4 OS=Homo sapiens GN=KCNN4 PE=1 SV=1 - [KCNN4_HUMAN]
Q15811	Intersectin-1 OS=Homo sapiens GN=ITSN1 PE=1 SV=3 - [ITSN1_HUMAN]
P57087	Junctional adhesion molecule B OS=Homo sapiens GN=JAM2 PE=1 SV=1 - [JAM2_HUMAN]
Q8N9B5	Junction-mediating and -regulatory protein OS=Homo sapiens GN=JMY PE=1 SV=2 - [JMY_HUMAN]
O75449	Katanin p60 ATPase-containing subunit A1 OS=Homo sapiens GN=KATNA1 PE=1 SV=1 - [KTNA1_HUMAN]
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1 - [KHDR1_HUMAN]
Q6UWL6	Kin of IRRE-like protein 2 OS=Homo sapiens GN=KIRREL2 PE=1 SV=2 - [KIRR2_HUMAN]
P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 - [KNG1_HUMAN]
A6PVL3	Kinocilin OS=Homo sapiens GN=KNCN PE=2 SV=1 - [KNCN_HUMAN]
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1 - [LANC2_HUMAN]
Q01650	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 - [LAT1_HUMAN]
Q9HAR2	Latrophilin-3 OS=Homo sapiens GN=LPHN3 PE=2 SV=2 - [LPHN3_HUMAN]
Q5TDP6	Lengsin OS=Homo sapiens GN=LGSN PE=1 SV=1 - [LGSN_HUMAN]
Q6P1M3	Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=1 SV=2 - [L2GL2_HUMAN]
P42702	Leukemia inhibitory factor receptor OS=Homo sapiens GN=LIFR PE=1 SV=1 - [LIFR_HUMAN]
P16150	Leukosialin OS=Homo sapiens GN=SPN PE=1 SV=1 - [LEUK_HUMAN]
Q7Z4I7	LIM and senescent cell antigen-like-containing domain protein 2 OS=Homo sapiens GN=LIMS2 PE=1 SV=1 - [LIMS2_HUMAN]
P06858	Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1 - [LIPL_HUMAN]
O75335	Liprin-alpha-4 OS=Homo sapiens GN=PPFIA4 PE=2 SV=3 - [LIPA4_HUMAN]
P01130	Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1 - [LDLR_HUMAN]
P98164	Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3 - [LRP2_HUMAN]
Q6UWN0	Ly6/PLAUR domain-containing protein 4 OS=Homo sapiens GN=LYPD4 PE=2 SV=2 - [LYPD4_HUMAN]
O60449	Lymphocyte antigen 75 OS=Homo sapiens GN=LY75 PE=1 SV=3 - [LY75_HUMAN]

Q13094	Lymphocyte cytosolic protein 2 OS=Homo sapiens GN=LCP2 PE=1 SV=1 - [LCP2_HUMAN]
P22897	Macrophage mannose receptor 1 OS=Homo sapiens GN=MRC1 PE=1 SV=1 - [MRC1_HUMAN]
Q8WXG6	MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2 - [MADD_HUMAN]
Q14680	Maternal embryonic leucine zipper kinase OS=Homo sapiens GN=MELK PE=1 SV=3 - [MELK_HUMAN]
O15232	Matrilin-3 OS=Homo sapiens GN=MATN3 PE=1 SV=2 - [MATN3_HUMAN]
P50281	Matrix metalloproteinase-14 OS=Homo sapiens GN=MMP14 PE=1 SV=3 - [MMP14_HUMAN]
Q9UHM6	Melanopsin OS=Homo sapiens GN=OPN4 PE=1 SV=1 - [OPN4_HUMAN]
Q5TCQ9	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 OS=Homo sapiens GN=MAGI3 PE=1 SV=2 - [MAGI3_HUMAN]
Q16819	Meprin A subunit alpha OS=Homo sapiens GN=MEP1A PE=1 SV=2 - [MEP1A_HUMAN]
Q14833	Metabotropic glutamate receptor 4 OS=Homo sapiens GN=GRM4 PE=2 SV=1 - [GRM4_HUMAN]
P41594	Metabotropic glutamate receptor 5 OS=Homo sapiens GN=GRM5 PE=1 SV=2 - [GRM5_HUMAN]
Q9H8M5	Metal transporter CNNM2 OS=Homo sapiens GN=CNNM2 PE=1 SV=2 - [CNNM2_HUMAN]
Q6P4Q7	Metal transporter CNNM4 OS=Homo sapiens GN=CNNM4 PE=1 SV=3 - [CNNM4_HUMAN]
Q687X5	Metalloreductase STEAP4 OS=Homo sapiens GN=STEAP4 PE=1 SV=1 - [STEA4_HUMAN]
Q9Y4B5	Microtubule cross-linking factor 1 OS=Homo sapiens GN=MTCL1 PE=1 SV=5 - [MTCL1_HUMAN]
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 - [MACF1_HUMAN]
P27816	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]
O15021	Microtubule-associated serine/threonine-protein kinase 4 OS=Homo sapiens GN=MAST4 PE=1 SV=3 - [MAST4_HUMAN]
Q8WXI7	Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2 - [MUC16_HUMAN]
Q86VL8	Multidrug and toxin extrusion protein 2 OS=Homo sapiens GN=SLC47A2 PE=1 SV=1 - [S47A2_HUMAN]
P21439	Multidrug resistance protein 3 OS=Homo sapiens GN=ABCB4 PE=1 SV=2 - [MDR3_HUMAN]
O75970	Multiple PDZ domain protein OS=Homo sapiens GN=MPDZ PE=1 SV=2 - [MPDZ_HUMAN]
O15146	Muscle, skeletal receptor tyrosine-protein kinase OS=Homo sapiens GN=MUSK PE=1 SV=1 - [MUSK_HUMAN]
Q9NZM1	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1 - [MYOF_HUMAN]
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]
Q13496	Myotubularin OS=Homo sapiens GN=MTM1 PE=1 SV=2 - [MTM1_HUMAN]
Q6T4R5	Nance-Horan syndrome protein OS=Homo sapiens GN=NHS PE=1 SV=2 - [NHS_HUMAN]
Q8NF91	Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=4 - [SYNE1_HUMAN]
Q8WXH0	Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3 - [SYNE2_HUMAN]
O95185	Netrin receptor UNC5C OS=Homo sapiens GN=UNC5C PE=2 SV=2 - [UNC5C_HUMAN]
Q8NC67	Neuropilin and tolloid-like protein 2 OS=Homo sapiens GN=NETO2 PE=1 SV=1 - [NETO2_HUMAN]
Q9P121	Neurotrimin OS=Homo sapiens GN=NTM PE=1 SV=1 - [NTRI_HUMAN]
P29474	Nitric oxide synthase, endothelial OS=Homo sapiens GN=NOS3 PE=1 SV=3 - [NOS3_HUMAN]
P26717	NKG2-C type II integral membrane protein OS=Homo sapiens GN=KLRC2 PE=1 SV=2 - [NKG2C_HUMAN]
Q96PE5	Opalin OS=Homo sapiens GN=OPALIN PE=2 SV=1 - [OPALI_HUMAN]
Q9HC10	Otoferlin OS=Homo sapiens GN=OTOF PE=1 SV=3 - [OTOF_HUMAN]
Q6ZRI0	Otogelin OS=Homo sapiens GN=OTOG PE=1 SV=3 - [OTOG_HUMAN]
A5PKW4	PH and SEC7 domain-containing protein 1 OS=Homo sapiens GN=PSD PE=1 SV=2 - [PSD1_HUMAN]
Q9NYI0	PH and SEC7 domain-containing protein 3 OS=Homo sapiens GN=PSD3 PE=1 SV=2 - [PSD3_HUMAN]
O60346	PH domain leucine-rich repeat-containing protein phosphatase 1 OS=Homo sapiens GN=PHLPP1 PE=1 SV=3 - [PHLP1_HUMAN]
Q70Z35	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens GN=PREX2 PE=2 SV=1 - [PREX2_HUMAN]
P42336	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform OS=Homo sapiens GN=PIK3CA PE=1 SV=2 - [PK3CA_HUMAN]
P42356	Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=3 - [PI4KA_HUMAN]
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1 - [P4K2A_HUMAN]
O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Homo sapiens GN=PIK3C2A PE=1 SV=2 - [P3C2A_HUMAN]
O00750	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta OS=Homo sapiens GN=PIK3C2B PE=1 SV=2 - [P3C2B_HUMAN]
O75747	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit gamma OS=Homo sapiens

	GN=PIK3C2G PE=1 SV=3 - [P3C2G_HUMAN]
Q99755	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha OS=Homo sapiens GN=PIP5K1A PE=1 SV=1 - [PI51A_HUMAN]
Q9H307	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 - [PININ_HUMAN]
Q16720	Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3 - [AT2B3_HUMAN]
P23634	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2 - [AT2B4_HUMAN]
P00747	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2 - [PLMN_HUMAN]
Q9HBL7	Plasminogen receptor (KT) OS=Homo sapiens GN=PLGRKT PE=1 SV=1 - [PLRKT_HUMAN]
Q9HCN6	Platelet glycoprotein VI OS=Homo sapiens GN=GP6 PE=1 SV=4 - [GPVI_HUMAN]
P16234	Platelet-derived growth factor receptor alpha OS=Homo sapiens GN=PDGFRA PE=1 SV=1 - [PGFRA_HUMAN]
Q9HCM2	Plexin-A4 OS=Homo sapiens GN=PLXNA4 PE=1 SV=4 - [PLXA4_HUMAN]
O15031	Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 - [PLXB2_HUMAN]
Q9Y4D7	Plexin-D1 OS=Homo sapiens GN=PLXND1 PE=1 SV=3 - [PLXD1_HUMAN]
Q8TDX9	Polycystic kidney disease protein 1-like 1 OS=Homo sapiens GN=PKD1L1 PE=1 SV=1 - [PK1L1_HUMAN]
Q7Z443	Polycystic kidney disease protein 1-like 3 OS=Homo sapiens GN=PKD1L3 PE=1 SV=1 - [PK1L3_HUMAN]
A8MYU2	Potassium channel subfamily U member 1 OS=Homo sapiens GN=KCNU1 PE=1 SV=2 - [KCNU1_HUMAN]
Q14721	Potassium voltage-gated channel subfamily B member 1 OS=Homo sapiens GN=KCNB1 PE=1 SV=2 - [KCNB1_HUMAN]
Q03721	Potassium voltage-gated channel subfamily C member 4 OS=Homo sapiens GN=KCNC4 PE=1 SV=2 - [KCNC4_HUMAN]
Q8TAE7	Potassium voltage-gated channel subfamily G member 3 OS=Homo sapiens GN=KCNG3 PE=1 SV=1 - [KCNG3_HUMAN]
Q8NCM2	Potassium voltage-gated channel subfamily H member 5 OS=Homo sapiens GN=KCNH5 PE=1 SV=3 - [KCNH5_HUMAN]
Q9NS40	Potassium voltage-gated channel subfamily H member 7 OS=Homo sapiens GN=KCNH7 PE=2 SV=2 - [KCNH7_HUMAN]
Q9NR82	Potassium voltage-gated channel subfamily KQT member 5 OS=Homo sapiens GN=KCNQ5 PE=1 SV=3 - [KCNQ5_HUMAN]
O60741	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1 OS=Homo sapiens GN=HCN1 PE=1 SV=3 - [HCN1_HUMAN]
Q9UL51	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 OS=Homo sapiens GN=HCN2 PE=1 SV=3 - [HCN2_HUMAN]
P54707	Potassium-transporting ATPase alpha chain 2 OS=Homo sapiens GN=ATP12A PE=1 SV=3 - [AT12A_HUMAN]
P01133	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2 - [EGF_HUMAN]
Q14005	Pro-interleukin-16 OS=Homo sapiens GN=IL16 PE=1 SV=4 - [IL16_HUMAN]
O14511	Pro-neuregulin-2, membrane-bound isoform OS=Homo sapiens GN=NRG2 PE=1 SV=1 - [NRG2_HUMAN]
Q8NBP7	Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN=PCSK9 PE=1 SV=3 - [PCSK9_HUMAN]
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 - [ADRM1_HUMAN]
Q8IVF2	Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 - [AHNK2_HUMAN]
P02760	Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1 - [AMBP_HUMAN]
Q9UPA5	Protein bassoon OS=Homo sapiens GN=BSN PE=2 SV=4 - [BSN_HUMAN]
Q9ULD6	Protein inturned OS=Homo sapiens GN=INTU PE=2 SV=2 - [INTU_HUMAN]
Q05655	Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2 - [KPCD_HUMAN]
Q96RT1	Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2 - [LAP2_HUMAN]
Q3SYG4	Protein PTHB1 OS=Homo sapiens GN=BBS9 PE=1 SV=1 - [PTHB1_HUMAN]
Q9HCY8	Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1 - [S10AE_HUMAN]
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 - [S10A8_HUMAN]
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]
P25815	Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2 - [S100P_HUMAN]
Q8TF72	Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2 - [SHRM3_HUMAN]
O94964	Protein SOGA1 OS=Homo sapiens GN=SOGA1 PE=1 SV=2 - [SOGA1_HUMAN]
Q8WWL2	Protein spire homolog 2 OS=Homo sapiens GN=SPIRE2 PE=1 SV=3 - [SPIR2_HUMAN]
Q9C0D5	Protein TANC1 OS=Homo sapiens GN=TANC1 PE=1 SV=3 - [TANC1_HUMAN]
Q9UPX0	Protein turtle homolog B OS=Homo sapiens GN=IGSF9B PE=2 SV=2 - [TUTLB_HUMAN]

Q9P2D8	Protein unc-79 homolog OS=Homo sapiens GN=UNC79 PE=2 SV=4 - [UNC79_HUMAN]
Q8N2C7	Protein unc-80 homolog OS=Homo sapiens GN=UNC80 PE=2 SV=2 - [UNC80_HUMAN]
P55085	Proteinase-activated receptor 2 OS=Homo sapiens GN=F2RL1 PE=1 SV=1 - [PAR2_HUMAN]
P20396	Pro-thyrotropin-releasing hormone OS=Homo sapiens GN=TRH PE=1 SV=1 - [TRH_HUMAN]
Q9Y5I1	Protocadherin alpha-11 OS=Homo sapiens GN=PCDHA11 PE=2 SV=1 - [PCDAB_HUMAN]
Q9UN72	Protocadherin alpha-7 OS=Homo sapiens GN=PCDHA7 PE=2 SV=1 - [PCDA7_HUMAN]
Q14517	Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 - [FAT1_HUMAN]
Q9NYQ8	Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2 - [FAT2_HUMAN]
Q08174	Protocadherin-1 OS=Homo sapiens GN=PCDH1 PE=1 SV=2 - [PCDH1_HUMAN]
O14917	Protocadherin-17 OS=Homo sapiens GN=PCDH17 PE=2 SV=2 - [PCD17_HUMAN]
Q9HCL0	Protocadherin-18 OS=Homo sapiens GN=PCDH18 PE=2 SV=3 - [PCD18_HUMAN]
Q8TAB3	Protocadherin-19 OS=Homo sapiens GN=PCDH19 PE=1 SV=3 - [PCD19_HUMAN]
Q96QE2	Proton myo-inositol cotransporter OS=Homo sapiens GN=SLC2A13 PE=1 SV=3 - [MYCT_HUMAN]
P16109	P-selectin OS=Homo sapiens GN=SELP PE=1 SV=3 - [LYAM3_HUMAN]
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]
Q9H1K0	Rabenosyn-5 OS=Homo sapiens GN=RBSN PE=1 SV=2 - [RBNS5_HUMAN]
P31751	RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2 - [AKT2_HUMAN]
P23468	Receptor-type tyrosine-protein phosphatase delta OS=Homo sapiens GN=PTPRD PE=1 SV=2 - [PTPRD_HUMAN]
P10586	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2 - [PTPRF_HUMAN]
Q92932	Receptor-type tyrosine-protein phosphatase N2 OS=Homo sapiens GN=PTPRN2 PE=1 SV=2 - [PTPR2_HUMAN]
Q16827	Receptor-type tyrosine-protein phosphatase O OS=Homo sapiens GN=PTPRO PE=1 SV=2 - [PTPRO_HUMAN]
O14924	Regulator of G-protein signaling 12 OS=Homo sapiens GN=RGS12 PE=1 SV=1 - [RGS12_HUMAN]
P49796	Regulator of G-protein signaling 3 OS=Homo sapiens GN=RGS3 PE=1 SV=2 - [RGS3_HUMAN]
O75787	Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=1 SV=2 - [RENR_HUMAN]
Q9NQC3	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2 - [RTN4_HUMAN]
P78363	Retinal-specific ATP-binding cassette transporter OS=Homo sapiens GN=ABCA4 PE=1 SV=3 - [ABCA4_HUMAN]
Q14BN4	Sarcolemmal membrane-associated protein OS=Homo sapiens GN=SLMAP PE=1 SV=1 - [SLMAP_HUMAN]
O43464	Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2 - [HTRA2_HUMAN]
Q9P0L2	Serine/threonine-protein kinase MARK1 OS=Homo sapiens GN=MARK1 PE=1 SV=2 - [MARK1_HUMAN]
Q9Y5S2	Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2 - [MRCKB_HUMAN]
Q9Y566	SH3 and multiple ankyrin repeat domains protein 1 OS=Homo sapiens GN=SHANK1 PE=1 SV=2 - [SHAN1_HUMAN]
Q9UPX8	SH3 and multiple ankyrin repeat domains protein 2 OS=Homo sapiens GN=SHANK2 PE=1 SV=3 - [SHAN2_HUMAN]
Q5BIV9	Shadow of prion protein OS=Homo sapiens GN=SPRN PE=2 SV=1 - [SPRN_HUMAN]
A6NMB1	Sialic acid-binding Ig-like lectin 16 OS=Homo sapiens GN=SIGLEC16 PE=2 SV=3 - [SIG16_HUMAN]
Q9BZZ2	Sialoadhesin OS=Homo sapiens GN=SIGLEC1 PE=1 SV=2 - [SN_HUMAN]
Q8IWY4	Signal peptide, CUB and EGF-like domain-containing protein 1 OS=Homo sapiens GN=SCUBE1 PE=1 SV=3 - [SCUB1_HUMAN]
P52630	Signal transducer and activator of transcription 2 OS=Homo sapiens GN=STAT2 PE=1 SV=1 - [STAT2_HUMAN]
O43166	Signal-induced proliferation-associated 1-like protein 1 OS=Homo sapiens GN=SIPA1L1 PE=1 SV=4 - [SI1L1_HUMAN]
Q9Y5Y9	Sodium channel protein type 10 subunit alpha OS=Homo sapiens GN=SCN10A PE=1 SV=2 - [SCNAA_HUMAN]
Q99250	Sodium channel protein type 2 subunit alpha OS=Homo sapiens GN=SCN2A PE=1 SV=3 - [SCN2A_HUMAN]
P35499	Sodium channel protein type 4 subunit alpha OS=Homo sapiens GN=SCN4A PE=1 SV=4 - [SCN4A_HUMAN]
Q14524	Sodium channel protein type 5 subunit alpha OS=Homo sapiens GN=SCN5A PE=1 SV=2 - [SCN5A_HUMAN]
Q9UQD0	Sodium channel protein type 8 subunit alpha OS=Homo sapiens GN=SCN8A PE=1 SV=1 - [SCN8A_HUMAN]
Q96EP9	Sodium/bile acid cotransporter 4 OS=Homo sapiens GN=SLC10A4 PE=1 SV=2 - [NTCP4_HUMAN]
P53794	Sodium/myo-inositol cotransporter OS=Homo sapiens GN=SLC5A3 PE=3 SV=2 - [SC5A3_HUMAN]

O60721	Sodium/potassium/calcium exchanger 1 OS=Homo sapiens GN=SLC24A1 PE=1 SV=1 - [NCKX1_HUMAN]
P05026	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1 - [AT1B1_HUMAN]
O00624	Sodium-dependent phosphate transport protein 3 OS=Homo sapiens GN=SLC17A2 PE=2 SV=2 - [NPT3_HUMAN]
Q13621	Solute carrier family 12 member 1 OS=Homo sapiens GN=SLC12A1 PE=1 SV=2 - [S12A1_HUMAN]
Q9H2X9	Solute carrier family 12 member 5 OS=Homo sapiens GN=SLC12A5 PE=2 SV=3 - [S12A5_HUMAN]
Q9UHW9	Solute carrier family 12 member 6 OS=Homo sapiens GN=SLC12A6 PE=1 SV=2 - [S12A6_HUMAN]
Q9Y666	Solute carrier family 12 member 7 OS=Homo sapiens GN=SLC12A7 PE=1 SV=3 - [S12A7_HUMAN]
Q9Y267	Solute carrier family 22 member 14 OS=Homo sapiens GN=SLC22A14 PE=2 SV=4 - [S22AE_HUMAN]
Q6T423	Solute carrier family 22 member 25 OS=Homo sapiens GN=SLC22A25 PE=2 SV=2 - [S22AP_HUMAN]
Q9Y694	Solute carrier family 22 member 7 OS=Homo sapiens GN=SLC22A7 PE=1 SV=1 - [S22A7_HUMAN]
Q9UHI7	Solute carrier family 23 member 1 OS=Homo sapiens GN=SLC23A1 PE=1 SV=3 - [S23A1_HUMAN]
Q9BXS9	Solute carrier family 26 member 6 OS=Homo sapiens GN=SLC26A6 PE=1 SV=1 - [S26A6_HUMAN]
Q9Y6L6	Solute carrier organic anion transporter family member 1B1 OS=Homo sapiens GN=SLCO1B1 PE=1 SV=2 - [SO1B1_HUMAN]
Q96BD0	Solute carrier organic anion transporter family member 4A1 OS=Homo sapiens GN=SLCO4A1 PE=1 SV=2 - [SO4A1_HUMAN]
P30626	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1 - [SORCN_HUMAN]
Q7Z614	Sorting nexin-20 OS=Homo sapiens GN=SNX20 PE=1 SV=1 - [SNX20_HUMAN]
P02549	Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=5 - [SPTA1_HUMAN]
Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTN1_HUMAN]
Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN]
P28290	Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=1 SV=3 - [SSFA2_HUMAN]
Q8WWQ8	Stabilin-2 OS=Homo sapiens GN=STAB2 PE=1 SV=3 - [STAB2_HUMAN]
Q9UBI4	Stomatin-like protein 1 OS=Homo sapiens GN=STOML1 PE=1 SV=1 - [STML1_HUMAN]
Q9Y5Y6	Suppressor of tumorigenicity 14 protein OS=Homo sapiens GN=ST14 PE=1 SV=2 - [ST14_HUMAN]
Q5SQN1	Synaptosomal-associated protein 47 OS=Homo sapiens GN=SNAP47 PE=1 SV=3 - [SNP47_HUMAN]
Q7L8C5	Synaptotagmin-13 OS=Homo sapiens GN=SYT13 PE=1 SV=1 - [SYT13_HUMAN]
Q86SS6	Synaptotagmin-9 OS=Homo sapiens GN=SYT9 PE=2 SV=1 - [SYT9_HUMAN]
Q4VX76	Synaptotagmin-like protein 3 OS=Homo sapiens GN=SYTL3 PE=2 SV=3 - [SYTL3_HUMAN]
Q9Y6H5	Synphilin-1 OS=Homo sapiens GN=SNCAIP PE=1 SV=2 - [SNCAP_HUMAN]
Q8N4C7	Syntaxin-19 OS=Homo sapiens GN=STX19 PE=1 SV=1 - [STX19_HUMAN]
Q9BPZ7	Target of rapamycin complex 2 subunit MAPKAP1 OS=Homo sapiens GN=MAPKAP1 PE=1 SV=2 - [SIN1_HUMAN]
Q7RTX0	Taste receptor type 1 member 3 OS=Homo sapiens GN=TAS1R3 PE=1 SV=2 - [TS1R3_HUMAN]
P59551	Taste receptor type 2 member 60 OS=Homo sapiens GN=TAS2R60 PE=2 SV=1 - [T2R60_HUMAN]
Q9NYW3	Taste receptor type 2 member 7 OS=Homo sapiens GN=TAS2R7 PE=1 SV=1 - [TA2R7_HUMAN]
P01730	T-cell surface glycoprotein CD4 OS=Homo sapiens GN=CD4 PE=1 SV=1 - [CD4_HUMAN]
Q6N022	Teneurin-4 OS=Homo sapiens GN=TENM4 PE=1 SV=2 - [TEN4_HUMAN]
Q63HR2	Tensin-2 OS=Homo sapiens GN=TNS2 PE=1 SV=2 - [TNS2_HUMAN]
O95049	Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=1 SV=3 - [ZO3_HUMAN]
O60603	Toll-like receptor 2 OS=Homo sapiens GN=TLR2 PE=1 SV=1 - [TLR2_HUMAN]
Q9NYK1	Toll-like receptor 7 OS=Homo sapiens GN=TLR7 PE=2 SV=1 - [TLR7_HUMAN]
Q9UKE5	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=1 SV=1 - [TNIK_HUMAN]
Q15582	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1 - [BGH3_HUMAN]
Q7Z2W7	Transient receptor potential cation channel subfamily M member 8 OS=Homo sapiens GN=TRPM8 PE=1 SV=2 - [TRPM8_HUMAN]
A2VDJ0	Transmembrane protein 131-like OS=Homo sapiens GN=KIAA0922 PE=1 SV=2 - [T131L_HUMAN]
Q86YD3	Transmembrane protein 25 OS=Homo sapiens GN=TMEM25 PE=1 SV=1 - [TMM25_HUMAN]
Q9HCN3	Transmembrane protein 8A OS=Homo sapiens GN=TMEM8A PE=1 SV=3 - [TMM8A_HUMAN]
Q9NP99	Triggering receptor expressed on myeloid cells 1 OS=Homo sapiens GN=TREM1 PE=1 SV=1 - [TREM1_HUMAN]
Q6ZMU5	Tripartite motif-containing protein 72 OS=Homo sapiens GN=TRIM72 PE=1 SV=2 - [TRI72_HUMAN]
P50591	Tumor necrosis factor ligand superfamily member 10 OS=Homo sapiens GN=TNFSF10 PE=1 SV=1 - [TNF10_HUMAN]

Q06187	Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3 - [BTK_HUMAN]
Q08881	Tyrosine-protein kinase ITK/TSK OS=Homo sapiens GN=ITK PE=1 SV=1 - [ITK_HUMAN]
P23458	Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2 - [JAK1_HUMAN]
Q6J9G0	Tyrosine-protein kinase STYK1 OS=Homo sapiens GN=STYK1 PE=1 SV=4 - [STYK1_HUMAN]
Q05209	Tyrosine-protein phosphatase non-receptor type 12 OS=Homo sapiens GN=PTPN12 PE=1 SV=3 - [PTN12_HUMAN]
Q9Y2R2	Tyrosine-protein phosphatase non-receptor type 22 OS=Homo sapiens GN=PTPN22 PE=1 SV=2 - [PTN22_HUMAN]
Q03405	Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1 - [UPAR_HUMAN]
O75445	Usherin OS=Homo sapiens GN=USH2A PE=1 SV=3 - [USH2A_HUMAN]
P46939	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 - [UTRO_HUMAN]
P35968	Vascular endothelial growth factor receptor 2 OS=Homo sapiens GN=KDR PE=1 SV=2 - [VGFR2_HUMAN]
Q14D04	Ventricular zone-expressed PH domain-containing protein homolog 1 OS=Homo sapiens GN=VEPH1 PE=2 SV=1 - [MELT_HUMAN]
P98155	Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR PE=1 SV=1 - [VLDLR_HUMAN]
P07225	Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1 - [PROS_HUMAN]
Q9Y698	Voltage-dependent calcium channel gamma-2 subunit OS=Homo sapiens GN=CACNG2 PE=1 SV=1 - [CCG2_HUMAN]
P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1 PE=1 SV=3 - [CA2D1_HUMAN]
Q13936	Voltage-dependent L-type calcium channel subunit alpha-1C OS=Homo sapiens GN=CACNA1C PE=1 SV=4 - [CAC1C_HUMAN]
Q01668	Voltage-dependent L-type calcium channel subunit alpha-1D OS=Homo sapiens GN=CACNA1D PE=1 SV=2 - [CAC1D_HUMAN]
P54284	Voltage-dependent L-type calcium channel subunit beta-3 OS=Homo sapiens GN=CACNB3 PE=1 SV=1 - [CACB3_HUMAN]
O00555	Voltage-dependent P/Q-type calcium channel subunit alpha-1A OS=Homo sapiens GN=CACNA1A PE=1 SV=2 - [CAC1A_HUMAN]
Q15878	Voltage-dependent R-type calcium channel subunit alpha-1E OS=Homo sapiens GN=CACNA1E PE=1 SV=3 - [CAC1E_HUMAN]
O43497	Voltage-dependent T-type calcium channel subunit alpha-1G OS=Homo sapiens GN=CACNA1G PE=2 SV=3 - [CAC1G_HUMAN]
O95180	Voltage-dependent T-type calcium channel subunit alpha-1H OS=Homo sapiens GN=CACNA1H PE=1 SV=4 - [CAC1H_HUMAN]
Q9P0X4	Voltage-dependent T-type calcium channel subunit alpha-1I OS=Homo sapiens GN=CACNA1I PE=1 SV=1 - [CAC1I_HUMAN]
Q14722	Voltage-gated potassium channel subunit beta-1 OS=Homo sapiens GN=KCNAB1 PE=1 SV=1 - [KCAB1_HUMAN]
Q8IWT6	Volume-regulated anion channel subunit LRRC8A OS=Homo sapiens GN=LRRC8A PE=1 SV=1 - [LRC8A_HUMAN]
Q7L1W4	Volume-regulated anion channel subunit LRRC8D OS=Homo sapiens GN=LRRC8D PE=1 SV=1 - [LRC8D_HUMAN]
Q8N8Y2	V-type proton ATPase subunit d 2 OS=Homo sapiens GN=ATP6V0D2 PE=2 SV=1 - [VA0D2_HUMAN]